SEQUENCE LISTING

<110> Codexis, Inc.
BONG, Yong Koy
CLAY, Michael D.
COLLIER, Steven J.
MIJTS, Benjamin
SMITH, Derek
VOGEL, Michael
ZHANG, Xiyun
ZHU, Jun
NAZOR, Jovana

<120> Synthesis of Prazole Compounds

<130> CX2-036WO1

<150> US 61/267,812
<151> 2009-12-08

<160> 268

<170> PatentIn version 3.5

<210> 1
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<213> Artificial Sequence

<220>
<223> Codon-optimized cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

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gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

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cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

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<212> PRT
<213> Acinetobacter sp NCIMB9871

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20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Phe
            420                 425                 430
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Thr Asn Leu Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Trp Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 3
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<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg      720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg      840
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gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

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gcgaatgcgt aa 1632

<210> 4
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

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Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380
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Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt      540
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cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

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gcgaatgcgt aa 1632

<210> 6
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Thr Arg Pro Asn Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
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Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Ile Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ser
            420                 425                 430

Gly Asn Ala Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Arg Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  7
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240
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aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

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gcgaatgcgt aa 1632

<210> 8
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

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Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
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Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305 310 315 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
420 425 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 9
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 9
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 10
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 10

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
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Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 11
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 11
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 12
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 12

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

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Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
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Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 13
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 13
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag ctggactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 14
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 14

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

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Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Trp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460
```

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 15
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 16
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 16

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

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Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415
```

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 17
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 17
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 18
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 18

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

```
Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380
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Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 19
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 19

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

ttaggtttgc tgtctgcacc taacctacca aatatcaagg gcatcaatca gtttaaaggc      480
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gcactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac caaacaacca 1620

gcgaatgcgt aa 1632

<210> 20
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 20

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

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Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Ala Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
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Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  21
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  21
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaacgttc aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180
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catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gcactgcacc atacttcccg ctggccggat gacgtgagtc ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctacaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 22
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 22

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Asn
20 25 30

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Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Ala Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
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```
Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 23
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 23
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg caggggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 24
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp

NCIMB9871

<400> 24

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

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

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
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Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 25
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 25
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggacg taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctaacgg tgtttcagcg tagtgcacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgg tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcagg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 26
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 26

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Asp Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

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Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Val Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Arg Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
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Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 27
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 27
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gccgtaaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 28
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 28

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445
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Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 29
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg agcgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tttaaacggt ccactggtta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagccccaac gttctgacat caaacaagca 1620

gcgaatgcgt aa 1632

<210> 30
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 30

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

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Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Ala Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415
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Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Leu Asn Gly Pro Leu
420 425 430

Val Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Pro Gln Arg Ser Asp Ile Lys Gln Ala Ala Asn Ala
530 535 540

<210> 31
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 32
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 32

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

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Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
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Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 33
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 33
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ataggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actgccaaag 600

aacctgacgg tgtttcagcg tagtgcacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt attataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga aaacgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 34
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 34

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Ala Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

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Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Ile Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Pro Lys Asn Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
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Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Glu Asn
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 35
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 35
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

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aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

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aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 36
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 36

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 37
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 37
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 38
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 38

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
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Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 39
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 39
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctacccc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actggtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 40
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 40

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Thr Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

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Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
```

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Trp Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 41
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 41
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa aaccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 42
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 42

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Lys Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445
```

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 43
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 43
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat 60

gcagctaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg aaacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gtgctgcacc atacttcccg ctggccggat gacgtgagtt ttgaagataa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgt cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtct gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtca gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg cggagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 44
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 44

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Ala Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Glu Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

```
Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Val Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Asp
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ser Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Leu Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Ser Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Ala Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
```

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 45
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 45
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctacccc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg cggagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 46
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 46

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

```
Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Thr Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Ala Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
```

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 47
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 47
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 48
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 48

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
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Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 49
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 49
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aggccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcagg gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgaaccagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgtacc taacgtgcca aatatcaagg gcatcaatca gtttaaaggc 480

gatctgcacc atacttcccg ctggccggat gacgtgagtt tagaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagccgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 50
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 50

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Gly Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

Tyr Val Gln Gly Pro Asp Val Arg Lys Tyr Leu Asn Gln Val Ala Glu
                85                  90                  95

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Val Pro Asn Val Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Asp Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Pro Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 51
<211> 1632

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 51
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 52
<211> 543
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 52

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240
```

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Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 53
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 53
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgttcc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtc tggaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 54
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 54

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Val Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

```
Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
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Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 55
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 55
atgtctacca agatggattt cgatgccatc gtgatcggtg ccggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtcggtttgc tgtctgtgcc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtc tggaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggtttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt acgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgggt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 56
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 56

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Val Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Leu Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Gly Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430
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Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 57
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 57
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 58
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 58

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 59
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 59
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 60
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 60

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
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Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  61
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  61
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgacgga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300
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aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 62
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 62

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
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Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  63
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  63
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

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gcgaatgcgt aa 1632

<210> 64
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 64

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1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
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Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 65
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tagaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

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aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 66

<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 66

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1               5                   10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240
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Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 67
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 67
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

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ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tagaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aagaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

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aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 68
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 68

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

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Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460
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Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 69
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 70
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 70

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430
```

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 71
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 71
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 72
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 72

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

```
Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380
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Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 73
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 73

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt      540
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gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacgcaaa ccgcggccaa cattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 74
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 74

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

```
Tyr Val Gln Gly Pro Asp Val Arg Lys Tyr Leu Gln Gln Val Ala Glu
                85                  90                  95

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
```

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Ala Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 75
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 75
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 76
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 76

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

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Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
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```
Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540

<210>  77
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871
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<400> 77
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggcg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 78
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 78

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
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Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 79
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 79
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggcg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc gctacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatgaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttatgatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 80
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 80

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala Arg Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Met Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

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Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Met Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Lys Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
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Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 81
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 81
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggcg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc gctacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatgaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttatgatc cagtataccg tcgaaaataa tgtgaaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 82
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 82

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala Arg Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Met Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

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Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Met Ile Gln Tyr Thr Val Glu Asn Asn Val Lys Ser Ile Glu Ala Thr
    450                 455                 460
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Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 83
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 83
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggcg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tgtcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 84
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 84

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

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Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Val
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415
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Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 85
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 85

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa      720

aacagtgcgc tggcctatgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780
```

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 86
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 86

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

```
Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380
```

```
Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 87
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 87

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480
```

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctgggg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 88
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 88

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

```
Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Trp Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
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```
Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  89
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  89
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180
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catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 90
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 90

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

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Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
```

```
Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540

<210>  91
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
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<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 91
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtatacca tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 92
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp

NCIMB9871

<400> 92

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
```

```
Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Ile Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 93
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 93
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg ctgtaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 94
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 94

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

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Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Cys Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Lys Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
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Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 95
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 95
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg caataatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 96
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 96

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Asn Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445
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Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 97
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 97

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa      720

aacagtgcgc tggcctatgg cgtgaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg      840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt      900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg      960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc     1020
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gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

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gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

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aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 98
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 98

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

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Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415
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Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 99
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

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agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 100
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 100

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

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Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Ser Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
```

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 101
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 101
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt tggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 102
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 102

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

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Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
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Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Phe Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 103
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 103
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccattcacca acctgccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagctgg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 104
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 104

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

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Phe
            420                 425                 430

Thr Asn Leu Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Trp Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 105
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 105
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtcgg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 106
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 106

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
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Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 107
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 107
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccccaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 108
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 108

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Pro Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

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Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
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Lys Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 109
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 109
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtcgg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 110
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 110

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445
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Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 111
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 111
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccacag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 112
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 112

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 113
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

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gcgaatgcgt aa 1632

<210> 114
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 114

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

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Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
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Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 115
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cagtaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttttgatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 116
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 116

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Ser Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
```

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Leu Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 117
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 117
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtc tggaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatc 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtcgg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 118
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 118

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540
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<210> 119
<211> 1632

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 119
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtc tggaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtcgg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 120
<211> 543
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 120

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240
```

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Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 121
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 121
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtc tggaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtcgg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 122
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 122

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

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Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
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Lys Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 123
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 123
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 124
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 124

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430
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Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 125
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 125
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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatc 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 126
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 126

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 127
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 127
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caagggaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatc 1200

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aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

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aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 128
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 128

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Gly Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
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Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 129
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 129
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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatc 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

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gcgaatgcgt aa 1632

<210> 130
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 130

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
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Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
370 375 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Leu Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 131
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 131

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

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ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

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aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

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gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

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aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 132
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 132

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
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Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Arg Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540
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<210> 133
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 133
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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

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aacagtgcgc tggggtatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

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aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcttgaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

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gcgaatgcgt aa 1632

<210> 134

<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 134

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225 230 235 240

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Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Leu Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 135
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatc gctattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

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aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

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attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgc gacgggtttt 1140

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attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

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gcgaatgcgt aa 1632

<210> 136
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 136

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Glu Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Arg
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

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Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Asp Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460
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Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

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

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

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attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

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gcgaatgcgt aa 1632

<210> 138
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 138

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430
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Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 139
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 139
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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcggcaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 140
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 140

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

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Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380
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Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Gly Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 141
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 141
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 142
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 142

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
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Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540


<210>  143
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  143
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga cgaggcaact      120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa      240
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tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggttatgg catcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcgtaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

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aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaaaattacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

ggcaatgcgt aa 1632

<210> 144
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 144

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

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Val Lys Ala Phe Asp Glu Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Ile Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Arg
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
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Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Asn
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Gly Asn Ala
    530                 535                 540


<210>  145
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871
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gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttttt 720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcgaat 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 146
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 146

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Phe
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
```

```
Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Asn
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540
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<210> 147
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 147
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgg tacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 148
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 148

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

```
Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Gly Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
530 535 540

<210> 149
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 149
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctacccc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg aggtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgg gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcgaac 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaaaactacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 150
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 150

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Thr Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

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

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Gly Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460
```

```
Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Asn
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Asn
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540
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<210> 151
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 151

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atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa      240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctacccc taactggcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg aggtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa      720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg      840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt      900

attaaaggta aaatcgcgtg catcgtcaaa gatcaggcga tcgcccaaaa actgatgccg      960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc     1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc     1080
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gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgg gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaaaactacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 152
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 152

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

```
Ser Thr Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

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

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Gln Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Gly Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415
```

```
Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Asn
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540
```

<210> 153
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 153

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atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa      240

tacgtggaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctacccc taactggcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg aggtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa      720

aacagtgcgc tgggttatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780
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gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgtg catcgtcaaa gatcaggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacttgc tgatctgcgg gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 154
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 154

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

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Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Thr Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

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

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Cys Ile Val Lys Asp Gln Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Leu Leu Ile Cys Gly Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380
```

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Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540


<210>  155
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcagg gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc      480
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gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca ccaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtggtctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 156
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 156

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

```
Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
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```
Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540


<210>  157
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  157
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtaggtg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180
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catttgtatt gttattcctg ggacaaggaa atgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcagg gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagta tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctatgg cgtcaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtat gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gagaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcgggtg acggcagcta taaacgcatt gatatccaag ggaaaaacgg tctggccatt 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgtttttatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagccg acaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caaatgcagg atttttgggg cgaacattcc aggcaaaaag 1500

aacaccgtgt acctgtattt gggtggtctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgtggg ctttgatatt cagctgcaac gttctgacac aaaacaacag 1620

gcgaatgcgt aa 1632

<210> 158
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 158

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

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Val Lys Ala Phe Asp Lys Ala Thr Asp Val Gly Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Met Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

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

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Tyr Gly Val Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Met Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
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```
Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Glu Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Gly Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Ile Asp Ile Gln Gly Lys Asn Gly Leu Ala Ile
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Phe Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Asp
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Val Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Gln Ala Asn Ala
    530                 535                 540


<210>  159
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
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<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

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aacatgttta tggttcatgg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 160
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp

NCIMB9871

<400> 160

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
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Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val His Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 161
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 161
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttcaggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 162
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 162

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

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Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Gln Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
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Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 163
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 163
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccacatgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 164
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 164

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro His
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445
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Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 165
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 165
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccaaaggcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 166
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 166

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

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Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415
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Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Lys
420 425 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 167
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 167
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

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agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 168
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 168

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

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Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
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Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Thr
420 425 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 169
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 169
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagatgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 170
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 170

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

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Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
```

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Asp
420 425 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 171
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 171
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccatgtgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 172
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 172

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

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285
```

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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Cys
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540

<210>  173
<211>  1632
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 173
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccaattgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 174
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 174

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
```

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Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ile
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 175
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 175
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccacttgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 176
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 176

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

```
Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
```

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 177
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 177
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccatatgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 178
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 178

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Tyr
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445
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Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 179
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 179
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccttta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 180
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 180

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
420 425 430

Phe Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 181
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 181
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccaaga actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 182
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 182

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

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Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
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Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
420 425 430

Lys Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 183
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 183
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagcctgga actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 184
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 184

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
```

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
420 425 430

Trp Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 185
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 185
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcgag atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 186
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 186

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

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Glu Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 187
<211> 1632

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagccct atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 188
<211> 543
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 188

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240
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Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Pro Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 189
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 189
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtgt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

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attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 190
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 190

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

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Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

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

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
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Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 191
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 191
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcattttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 192
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 192

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

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe His Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430
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Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 193
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 193
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttatatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 194
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 194

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Tyr Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
420 425 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 195
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 195
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgtttttgg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 196
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 196

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Trp Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
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Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
420 425 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 197
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 197
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

catgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

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agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 198
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 198

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met His Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
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Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  199
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  199
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 200
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 200

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
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Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Ala Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 201
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 201
atgtctcaga agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatcgcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 202

<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 202

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225 230 235 240

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Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Ser Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 203
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 203
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcacttcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 204
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 204

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

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Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Leu Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460
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Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 205
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 205
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcagatcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 206
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 206

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Asp Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430
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Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 207
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 207
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcaaaacg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcaacta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccagccgcta actccccgcc tagcattgaa 1320

agtcaagttg aatggattag cgatactatc cagtataccg tcgaaaataa cgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagcctagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 208
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 208

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

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

```
Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Lys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380
```

```
Gly Asn Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Ala
            420                 425                 430

Ala Asn Ser Pro Pro Ser Ile Glu Ser Gln Val Glu Trp Ile Ser Asp
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 209
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 209

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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

ttaggtttgc tgtctgcacc taacatgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt      540
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gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 210
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 210

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

```
Tyr Val Gln Gly Pro Asp Val Arg Lys Tyr Leu Gln Gln Val Ala Glu
                85                  90                  95

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Met Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
```

```
Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540


<210>  211
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variant of cyclohexanone monooxygenase from Acinetobacter sp
       NCIMB9871

<400>  211
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240
```

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtct gcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 212
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 212

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

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Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Leu Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
```

```
Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 213
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 213
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgg cttctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 214
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 214

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Ala
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270
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Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 215
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 215
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gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt taactttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 216
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 216

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

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Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Asn Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
```

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 217
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 217
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtgtcc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 218
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 218

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Val Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

```
Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460
```

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Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 219
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 219

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atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

ttaggtaacc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg      720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg      840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt      900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg      960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc     1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc     1080
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gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt actttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 220
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 220

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Asn Leu
130 135 140

```
Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415
```

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
530 535 540

<210> 221
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 221
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggctttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagttc aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt tcgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtgcccag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgtttgg 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tgccacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg taaccgtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactgctga actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagcttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacat caaacaacca 1620

gcgaatgcgt aa 1632

<210> 222
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 222

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Gln Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

```
Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Ala Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Trp
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ala
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380
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Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Thr Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Leu Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Ala Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Ile Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 223
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 223

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atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat       60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

ttaggtttgc tgtctgcacc taactttcca aatatcaagg gcatcaatca gtttaaaggc      480
```

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 224
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 224

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

```
Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Phe Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
```

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 225
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 225
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

ttaggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgggt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 226
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 226

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

```
Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Leu Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300
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Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Gly Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 227
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 227
atgtctacca agatggattt cgatgccatc gtgatcggtg ccggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtcggtttgc tgtctgtgcc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtc tggaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tgggtttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt acgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgggt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggtttttgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagagcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 228
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp

NCIMB9871

<400> 228

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Val Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Leu Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Gly Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
```

```
Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Leu Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Gly Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Ser Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 229
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 229
atgtctacca agatggattt cgatgccatc gtgatcggtg ggggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttctctacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttctggg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 230
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 230

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Gly Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

```
Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Ser Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Leu Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495
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Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 231
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 231
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttatattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 232
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 232

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

```
Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445
```

```
Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
                485                 490                 495

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 233
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 233

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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact      120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc      180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa      240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta      300

aaaaaaagct accagttcaa caccgcagtc caatctgccc actacaacga agcggacgct      360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc      420

gtgggtttgc tgtctgcacc taactggcca aatatcaagg gcatcaatca gtttaaaggc      480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt      540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag      600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg      660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa      720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg      780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg      840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt      900

attaaaggta aaatcgcgga gatcgtcaaa gatccggcga tcgcccaaaa actgatgccg      960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc     1020
```

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta tgttcgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

atgaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acttttattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 234
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 234

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Gln Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

```
Ser Ala Pro Asn Trp Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Glu Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Val Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415
```

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

Met Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Phe Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 235
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 235
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccgaggg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 236
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 236

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

```
Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Glu Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
```

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 237
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 237
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcccatgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 238
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 238

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

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Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala His Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335
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Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 239
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 239
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcccaggg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 240
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 240

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Gln Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540

<210>  241
<211>  1632
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 241
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctcggg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 242
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 242

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Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1               5                  10                  15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Ser Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255
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Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525
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Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 243
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 243
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggtca gcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 244
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 244

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

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Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Gln Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
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Lys Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 245
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 245
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcctgggg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 246
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 246

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

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Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Trp Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445
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Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 247
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 247
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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttggg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

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gcgaatgcgt aa 1632

<210> 248
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 248

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Gly Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
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<210> 249
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<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

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attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

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gcgaatgcgt aa 1632

<210> 250
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 250

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

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Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Gly Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365
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Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

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<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

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attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

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aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

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gcgaatgcgt aa 1632

<210> 252
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 252

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

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

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Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Arg Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
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Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

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<212> DNA
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<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

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gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

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ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

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gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 254
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 254

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

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Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
            20                  25                  30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
        35                  40                  45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Ser Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285
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Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
        515                 520                 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
    530                 535                 540
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<210> 255
<211> 1632

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 255
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

gctgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 256
<211> 543
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 256

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
210 215 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225 230 235 240

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Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Ala Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
            500                 505                 510
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Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 257
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 257
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

agtgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 258
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 258

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
165 170 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
180 185 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
195 200 205

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Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Ser Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
        435                 440                 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
    450                 455                 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465                 470                 475                 480
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Lys Thr Leu Phe Pro Lys Ala Gln Cys Arg Ile Phe Gly Ala Asn Ile
485 490 495

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 259
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 259
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcaag ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc caagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 260
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 260

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
130 135 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145 150 155 160

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Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
                405                 410                 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
            420                 425                 430
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Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 261
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 261
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gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc cttttgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 262
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 262

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
100 105 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
115 120 125

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Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
        355                 360                 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
    370                 375                 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385                 390                 395                 400
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Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 263
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 263
atgtctacca agatggattt cgatgccatc gtgatcggtg caggttttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggccttcgg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc cctgtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 264
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 264

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
50 55 60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65 70 75 80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Phe Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
                325                 330                 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
            340                 345                 350
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Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 265
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 265
atgtctacca agatggattt cgatgccatc gtgatcggtg caggatttgg cggtctgtat 60

gccgttaaaa aactgcgcga tgaactggag ctgaaagtta aagccttcga caaggcaact 120

gacgtagcgg gtacatggta ctggaaccgc tacccgggtg cactgaccga taccgaaacc 180

catttgtatt gttattcctg ggacaaggaa ctgttgcaga gtttggaaat caaaaagaaa 240

tacgtgcaag gtccagacgt gcgcaaatat ctgcagcagg ttgccgaaaa acacgactta 300

aaaaaaagct accagttcaa caccgcagtc acatctgccc actacaacga agcggacgct 360

ctgtgggaag taactacgga atacggggat aagtacaccg cacgtttcct gattactgcc 420

gtgggtttgc tgtctgcacc taacctgcca aatatcaagg gcatcaatca gtttaaaggc 480

gaactgcacc atacttcccg ctggccggat gacgtgagtt ttgaaggcaa acgtgtgggt 540

gtgatcggca caggctctac cggcgtgcaa gttatcacgg cagtggcgcc actggccaag 600

cacctgacgg tgtttcagcg tagtccgcag tactcggtcc cgatcggtaa cgatccactg 660

agcgaagaag acgtcaagaa gatcaaagat aactatgata aaatctggga tggtgttaaa 720

aacagtgcgc tggcccgggg cctgaatgaa tctactgtgc cggccatgtc cgtaagtgcg 780

gaagagcgta aagcggtttt tgagaaggcg tggcaaaccg gcggtggttt tcgttttatg 840

ttcgaaacct ttggtgatat tataacgaac atggaagcta acattgaggc acaaaatttt 900

attaaaggta aaatcgcgcg tatcgtcaaa gatccggcga tcgcccaaaa actgatgccg 960

caggatctgt acgcatgtcg ccctctgtgt gactccgggt actataatac gttcaatcgc 1020

gacaacgtac gtctggagga tgtcaaagca aatccgatcg tcgagatcac cgaaaacggc 1080

gtgaaactgg aaaacggcga tttcgtggag ctggacatgc tgatctgcgc gacgggtttt 1140

gatgcggtag acggcagcta taaacgcatg gatatccaag ggaaaaacgg tctggccatg 1200

aaggattact ggaaagaggg cccgtctagc tacatgggcg tagcagtgaa taattaccca 1260

aacatgttta tggttttcgg tccaaacggt ccactggcta actccccgcc tatcattgaa 1320

agtcaagttg aatggattag cgttactatc cagtataccg tcgaaaataa tgtggaatct 1380

attgaagcca cgaaggaagc ggaggaacag tggacccaaa cctgcgccaa tattgcggag 1440

aaaaccctgt ttccaaaagc ccagtgcagg atttttgggg cgaacattcc aggcaagaag 1500

aacaccgtgt acctgtattt gggtgggctg aaagagtacc gctcagtttt ggcgaattgt 1560

aaaaatcatg cgtatgaagg ctttgatatt cagctgcaac gttctgacac aaaacaacca 1620

gcgaatgcgt aa 1632

<210> 266
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of cyclohexanone monooxygenase from Acinetobacter sp NCIMB9871

<400> 266

Met Ser Thr Lys Met Asp Phe Asp Ala Ile Val Ile Gly Ala Gly Phe
1 5 10 15

Gly Gly Leu Tyr Ala Val Lys Lys Leu Arg Asp Glu Leu Glu Leu Lys
20 25 30

Val Lys Ala Phe Asp Lys Ala Thr Asp Val Ala Gly Thr Trp Tyr Trp
35 40 45

```
Asn Arg Tyr Pro Gly Ala Leu Thr Asp Thr Glu Thr His Leu Tyr Cys
    50                  55                  60

Tyr Ser Trp Asp Lys Glu Leu Leu Gln Ser Leu Glu Ile Lys Lys Lys
65                  70                  75                  80

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

Lys His Asp Leu Lys Lys Ser Tyr Gln Phe Asn Thr Ala Val Thr Ser
            100                 105                 110

Ala His Tyr Asn Glu Ala Asp Ala Leu Trp Glu Val Thr Thr Glu Tyr
        115                 120                 125

Gly Asp Lys Tyr Thr Ala Arg Phe Leu Ile Thr Ala Val Gly Leu Leu
    130                 135                 140

Ser Ala Pro Asn Leu Pro Asn Ile Lys Gly Ile Asn Gln Phe Lys Gly
145                 150                 155                 160

Glu Leu His His Thr Ser Arg Trp Pro Asp Asp Val Ser Phe Glu Gly
                165                 170                 175

Lys Arg Val Gly Val Ile Gly Thr Gly Ser Thr Gly Val Gln Val Ile
            180                 185                 190

Thr Ala Val Ala Pro Leu Ala Lys His Leu Thr Val Phe Gln Arg Ser
        195                 200                 205

Pro Gln Tyr Ser Val Pro Ile Gly Asn Asp Pro Leu Ser Glu Glu Asp
    210                 215                 220

Val Lys Lys Ile Lys Asp Asn Tyr Asp Lys Ile Trp Asp Gly Val Lys
225                 230                 235                 240

Asn Ser Ala Leu Ala Arg Gly Leu Asn Glu Ser Thr Val Pro Ala Met
                245                 250                 255

Ser Val Ser Ala Glu Glu Arg Lys Ala Val Phe Glu Lys Ala Trp Gln
            260                 265                 270

Thr Gly Gly Gly Phe Arg Phe Met Phe Glu Thr Phe Gly Asp Ile Ile
        275                 280                 285

Thr Asn Met Glu Ala Asn Ile Glu Ala Gln Asn Phe Ile Lys Gly Lys
    290                 295                 300

Ile Ala Arg Ile Val Lys Asp Pro Ala Ile Ala Gln Lys Leu Met Pro
305                 310                 315                 320
```

Gln Asp Leu Tyr Ala Cys Arg Pro Leu Cys Asp Ser Gly Tyr Tyr Asn
325 330 335

Thr Phe Asn Arg Asp Asn Val Arg Leu Glu Asp Val Lys Ala Asn Pro
340 345 350

Ile Val Glu Ile Thr Glu Asn Gly Val Lys Leu Glu Asn Gly Asp Phe
355 360 365

Val Glu Leu Asp Met Leu Ile Cys Ala Thr Gly Phe Asp Ala Val Asp
370 375 380

Gly Ser Tyr Lys Arg Met Asp Ile Gln Gly Lys Asn Gly Leu Ala Met
385 390 395 400

Lys Asp Tyr Trp Lys Glu Gly Pro Ser Ser Tyr Met Gly Val Ala Val
405 410 415

Asn Asn Tyr Pro Asn Met Phe Met Val Phe Gly Pro Asn Gly Pro Leu
420 425 430

Ala Asn Ser Pro Pro Ile Ile Glu Ser Gln Val Glu Trp Ile Ser Val
435 440 445

Thr Ile Gln Tyr Thr Val Glu Asn Asn Val Glu Ser Ile Glu Ala Thr
450 455 460

Lys Glu Ala Glu Glu Gln Trp Thr Gln Thr Cys Ala Asn Ile Ala Glu
465 470 475 480

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

Pro Gly Lys Lys Asn Thr Val Tyr Leu Tyr Leu Gly Gly Leu Lys Glu
500 505 510

Tyr Arg Ser Val Leu Ala Asn Cys Lys Asn His Ala Tyr Glu Gly Phe
515 520 525

Asp Ile Gln Leu Gln Arg Ser Asp Thr Lys Gln Pro Ala Asn Ala
530 535 540

<210> 267
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of KRED from Lactobacillus kefiri

<400> 267
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60

ttggcgatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120

gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180

cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240

ttcggcccgg ttacgaccgt cgtgaacaat gcagggattt tcgtttataa aagcgttgaa 300

gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360

ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420

atgagcagta ttgaggggct ggtaggcgat ccgacgggtg gggcatacaa cgcttccaag 480

ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540

gtgcgtgtca acacagtaca tccgggctat atcaagaccc cgctggtcga tgatctggaa 600

ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660

aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720

gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 268
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of KRED from Lactobacillus kefiri

<400> 268

Met Thr Asp Arg Leu Lys Gly Lys Val Ala Ile Val Thr Gly Gly Thr
1 5 10 15

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

Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35 40 45

Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50 55 60

Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65 70 75 80

Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Phe Val Tyr
85 90 95

Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100 105 110

Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115 120 125

```
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
    130                 135                 140

Glu Gly Leu Val Gly Asp Pro Thr Gly Gly Ala Tyr Asn Ala Ser Lys
145                 150                 155                 160

Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
                165                 170                 175

Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
            180                 185                 190

Thr Pro Leu Val Asp Asp Leu Glu Gly Ala Glu Glu Met Met Ser Gln
        195                 200                 205

Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
    210                 215                 220

Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225                 230                 235                 240

Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
                245                 250
```