SEQUENCE LISTING

<110> CODEXIS, INC.
ALVIZO, OSCAR
MAYO, MELISSA ANN
MOORE, JEFFREY C.

<120> ENGINEERED IMINE REDUCTASES AND METHODS FOR THE REDUCTIVE AMINATION OF KETONE AND AMINE COMPOUNDS

<130> CX2-145USP1

<140> 15/519,949
<141>

<150> 62/084,037
<151> 2014-11-25

<160> 1300

<210> 1
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1
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gcctatttag cattgaaggg ccagagtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa atatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcaacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaag tatgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtaaatg cgataaaagg cgccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacg tggctgtcga aaacgtgttg catacttcgc tgactaatgt gaacgctgta 600
atgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccaa 660
tattatctgg aggggattac gccatcagtc gggagtcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgcga atggtacaag 780
gaaagttacg gccagtcacc ggccacaatt tatgaagcgg tgcagggtaa tcctgcttat 840
cgcggcattg cgggacctat taaccttaac acgcgctact tcttcgagga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gcagtgaatg tgcctacccc acttatcgat 960
gctgttcttg acttgatcag ttcgctgata gacacggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcgggca taagaagtgc tgttgag 1077

<210> 2
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 2

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1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Ser Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Asn Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Ser Met Leu Phe Thr Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Asn Ala Ile Lys Gly Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Val Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Val Asn Ala Val Met His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Leu Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ser Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Tyr Lys Glu Ser Tyr Gly Gln Ser Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Val Gln Gly Asn Pro Ala Tyr Arg Gly Ile Ala Gly Pro Ile Asn
        275                 280                 285
Leu Asn Thr Arg Tyr Phe Phe Glu Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Ala Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Asp Leu Ile Ser Ser Leu Ile Asp Thr Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Gly Ile Arg Ser Ala Val Glu
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<210> 3
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 4
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 4
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His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240

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Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 5
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
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gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 6
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 6
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Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
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His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 7
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

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cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 8
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 8

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 9
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccatggac 480
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cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgatgctgta 600
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tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 10
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 10
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Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
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```
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 11
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 11
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 12
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 12
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 13
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 13
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtacaat ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 14
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 14
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 15
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 15
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

```
tggtgccgct ccgagagacc aggacaggtt acggtaaatt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 16
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 16

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

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 17
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 17
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtacgtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 18
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 18
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 19
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 19
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccatggac 480
tttgcatgtc tcccagcgac aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gcacaacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 20
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

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

<210> 21
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 21

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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtagaat ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 22
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 22

```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 23
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 23
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 24
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 24
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 25
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 25
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 26
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 26
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 27
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 27
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
```

```
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077


<210> 28
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 28
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
```

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 29
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 29
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcctagtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 30
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 30
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 31
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 31
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
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ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 32
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 32
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 33
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 33
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 34
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 34
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 35
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 35
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 36
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 36
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 37
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 37
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 38
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 38
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

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Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 39
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 39
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagaccgc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 40
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 41
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 41
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 42
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 42
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160

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Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 43
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 43
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 44

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 44
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 45
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 45
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 46
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 46
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 47
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 47
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 48
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 48
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 49
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 49
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgt gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 50
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Cys Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 51
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 51
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 52
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 52
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Cys Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 53
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 53
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc atggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 54
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 54
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val His Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 55
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 55
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcctagtgc taggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 56
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 56
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Leu Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 57
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 57
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc ttggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 58
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 58
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Leu Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 59
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 59
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 60
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 60

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

<210> 61
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 61
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 62
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 62

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 63
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 63
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc taggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 64
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 64
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 65
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 65
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagaccgc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 66
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 66

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

```
Glu Trp Val Lys His Ser Cys Gly Gln Thr Ala Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 67
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 67
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 68
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 68
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 69
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 69
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 70
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 71
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 71
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
ctcggtgtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 72
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 72
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 73
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 73
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 74
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 74
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 75
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 75
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc ttggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 76
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 76
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 77
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 77
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 78
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 78
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 79
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 79
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagaccgc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 80
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 80
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 81
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 81
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 82
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 82
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 83
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 83
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtgc ttggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 84
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 84
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Cys Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Leu Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 85
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 85
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
```

```
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 86
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 86

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

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 87
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 87
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcctagtgc atggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 88
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 88
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val His Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 89
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 89
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtgc atggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 90
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

Glu Ile Arg Ser Ala Val Glu
        355

<210> 91
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 91
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aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagaccgc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcggtgtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 92
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 92
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

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Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Ala Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 93
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 93
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 94
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 94
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Cys Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 95
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 95
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgctgcgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 96
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 96
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

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Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Cys Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 97
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 97
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
cattcttgtg gcgttacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 98
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 98
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Met Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Val Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 99
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 99
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgtgga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 100
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

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Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Val
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 101
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 101
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcggtgtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 102

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 102
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 103
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 103
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtgc atggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 104
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 104
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 105
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 105
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaag 780
catagttgtg gcgttacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtgt gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 106
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 106
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Val Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Cys Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 107
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 107
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
cattcttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 108
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 108
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

```
Ser Leu Thr Asn Met Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 109
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 109
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcctagtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 110
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 111
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 111
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctccga atgggttaag 780
catgtgtgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 112
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 112
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Met Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245                 250                 255
Glu Trp Val Lys His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 113
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 113
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat ggaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggtgtga gtggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 114
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 114
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Met Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 115
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 115
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
aatctagtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 116
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 116
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Cys Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Asp Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Gln Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Asn Leu Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 117
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 117
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
ccactagtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 118
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 118

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

<210> 119
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 119
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtgc acctgtgctg 840
cgcctagtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 120
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 120

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Ala Pro Val Leu Arg Leu Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 121
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 121
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg atgggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcctagtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 122
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 122
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 123
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 123
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct ttgccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtaggtt ttataacact ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgatgctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccag 660
tattataccg aggggattac gccatcagtc ggggcgcttt gtgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
catagttgtg gccagacccc ggccacaatt tatgatgcga tgcagggtct gcctgtgctg 840
cgcctagtgc aaggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 124
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 124

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

```
Glu Trp Val Lys His Ser Cys Gly Gln Thr Pro Ala Thr Ile Tyr Asp
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Leu Val Gln Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 125
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 125
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 126
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 126
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 127
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 127
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 128
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 128

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

```
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 129
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 129
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 130
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 130
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 131
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 131
atgatcgagt caaaaacata cgccggtttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atggatgaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 132
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 132
Met Ile Glu Ser Lys Thr Tyr Ala Gly Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Met Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 133
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 133
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgaa 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 134
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 134
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 135
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 135
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aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
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cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgaaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 136
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 136
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Glu Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 137
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 137
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 138
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 138
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 139
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 139
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attaatcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 140
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 141
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 141
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtacttt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 142
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 142
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 143
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 143
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
```

attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 144
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 144
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 145
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 145
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgcactg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 146
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 146
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 147
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 147
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tccttatctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
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ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 148
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 148
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Tyr Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 149
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 149
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 150
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

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Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 151
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 151
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctagt 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 152
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 152
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 153
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 153
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaatgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 154
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 154
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

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Glu Arg Pro Gly Gln Val Thr Val Met Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 155
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 155
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctcatctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 156
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 156
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 157
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 157
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaatgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 158
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 158
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Met Phe Ile Asn Leu Ala Met Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 159
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 159
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atggattaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 160

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 161
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 161
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccaa tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 162
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 162
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

```
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Asn Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 163
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 163
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccat tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 164
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 164
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ile Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 165
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 165
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccc atgggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 166
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 166
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr His
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 167
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 167
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctggga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 168
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 168
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Trp
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 169
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 169
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 170
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 171
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 171
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgaa 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 172
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 172
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 173
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 173
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 174
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 174
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 175
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 175
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 176
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 176

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

<210> 177
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 177
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 178
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 178
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 179
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 179
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 180
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 180
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 181
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 181
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagccagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 182
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 182

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

```
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Tyr Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 183
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 183
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagccagg gccagaccac tgccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 184
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 184
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 185
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 185
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aagggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atggatgaga 780
agaagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 186
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 186

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

```
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 187
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 187
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 188
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 188
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 189
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 189
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
```

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attaaccagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 190
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 191
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 191
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 192
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 192
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 193
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 193
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 194
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 194
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Tyr Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 195
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 195
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 196
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 196
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 197
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 197
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 198
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 198
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 199
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 199
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 200
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 200
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 201
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 201
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aagggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atggattaaa 780
```

agaagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 202
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 202
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Ile Lys Arg Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 203
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 203
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagccagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 204
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 204
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 205
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 205
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtactgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaaa 780
agaagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 206
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 206
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Arg Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 207
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 207
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagccagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 208
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 208
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 209
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 209
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
```

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 210
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 211
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 211
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 212
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 212
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 213
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 213
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagccagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 214
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 214
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 215
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 215
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
attagccagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 216
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 216
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 217
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 217
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatacg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 218

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 218
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Val Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 219
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 219
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 220
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 220
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 221
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 221
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctaacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 222
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 222
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro Asn Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 223
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 223
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 224
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 224
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 225
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 225
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 226
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 226
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245   250   255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 227
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 227
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attaaccagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 228
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 228
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Asn Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 229
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 229
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 230
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 231
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 231
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctggga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 232
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 232
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Trp
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 233
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 233
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgaa 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctaacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 234
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 234

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

<210> 235
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 235
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 236
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 236

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 237
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 237
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctggga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 238
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 238
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 239
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 239
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attaaccagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctaacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 240
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 240

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

```
Glu Trp Val Lys Ile Asn Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Asn Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 241
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 241
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 242
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 242
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 243
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 243
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaatgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagccagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 244
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 244

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

```
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 245
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 245
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccaa tgccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 246
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 246
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 247
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 247
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

```
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggtgaga 780
agaagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggcacga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 248
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 248

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

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 249
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 249
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagagtaa tcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 250
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 250
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 251
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 251
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctttgctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 252
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 252
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Leu Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 253
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 253
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctggga atgggttaag 780
attagtcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tccttacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 254
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 254
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 255
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 255
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
```

tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagaccag tgccacaatt tatgaagcga tgcagggtaa tcctaacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 256
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 256
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Asn Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 257
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 257
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atggattaaa 780
agaagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 258
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 258
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Ile Lys Arg Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 259
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 259
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
```

attagtcagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 260
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 261
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 261
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaaa 780
agaagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgtcctg 840
cgcggcacga gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 262
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 262
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Arg Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 263
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 263
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 264
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 264
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 265
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 265
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agactgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc ggccacaatt tatgaagcga tgcagggtaa tcctgctctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 266
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Thr Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro Ala Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 267
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 267
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgaa 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
attagtcagg gccagacccc agccacaatt tatgaagcga tgcagggtaa tcctgttctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 268
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 268
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Ser Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 269
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 269
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 270
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 270
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 271
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 271
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 272
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 272
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245   250   255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 273
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 273
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 274
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Met Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 275
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 275
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 276

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 276
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Met Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 277
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 277
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
atatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 278
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 278
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

```
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Met Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 279
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 279
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
agatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 280
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 281
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 281
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 282
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 282
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

```
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Met Lys Arg Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 283
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 283
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 284
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 284
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245   250   255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 285
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 285
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 286
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 286
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Met Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 287
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 287
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggattaag 780
atatttcagg gccagaccta tgcaacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 288
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 288
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245   250   255
Glu Trp Ile Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 289
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 289
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatacg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 290
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 291
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 291
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 292
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 292

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

<210> 293
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 293
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 294
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 294
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Leu Val Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 295
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 295
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatacg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
agatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 296
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 296
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 297
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 297
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 298
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 298

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

```
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 299
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 299
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggattaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 300
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 300
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 301
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 301
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatacg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 302
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 302
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Val Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 303
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 303
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggattaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 304
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 304
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 305
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 305
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420

tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 306
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 306
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
245 250 255
Glu Trp Met Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 307
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 307
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggattaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 308
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 308
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 309
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 309
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 310
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

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

<210> 311
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 311
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 312
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 312
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 313
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 313
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660

tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 314
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 314
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Met Lys Arg Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 315
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 315
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
atatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 316
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 316
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Met Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 317
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 317
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
```

```
atatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 318
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 318

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

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 319
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 319
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 320
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 320
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 321
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 321
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatacg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 322
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 322
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Val Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 323
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 323
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 324
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 324
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 325
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 325
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 326
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 326
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Met Lys Arg Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 327
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 327
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggtgaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 328
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 328
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Ser Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Val Lys Arg Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 329
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 329
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 330
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 331
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 331
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 332
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 332
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160

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Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 333
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 333
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatact ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 334

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 335
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 335
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 336
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 336
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 337
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 337
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atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgg ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 338
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 338
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Leu Val Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 339
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 339
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 340
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 340
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

```
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 341
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 341
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
agatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 342
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 342
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245   250   255
Glu Trp Val Lys Arg Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 343
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 343
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggattaag 780
atatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 344
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 344
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205

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Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Glu Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Ile Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 345
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 345
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtattgt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaag 780
atttttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 346
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 346
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Leu Phe Ile Asn Leu Ala Met Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245   250   255
Glu Trp Val Lys Ile Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 347
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 347
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggatgaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 348
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 348
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Asn Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Cys
                245                 250                 255
Glu Trp Met Lys Arg Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 349
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 349
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gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 350
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 350

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

<210> 351
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 351
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atggatgaag 780
agatttcagg gccagacctc tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 352
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 352

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
                245                 250                 255
Glu Trp Met Lys Arg Phe Gln Gly Gln Thr Ser Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 353
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 353
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgcaaat ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttcc 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atggattaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 354
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 354
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 355
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 355
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctgtga atgggttaag 780
agatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 356
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 356

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

```
Glu Trp Val Lys Arg Phe Gln Gly Gln Thr Tyr Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Asn Pro His Leu Arg Gly Thr Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 357
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 357
```
atgatcgagt caaaaacata cgccgttttg ggattaggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaatct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
ttgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgag 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgagga atgggtgaag 780
atatttcagg gccagaccta tgccacaatt tatgaagcga tgcagggtaa tcctcacctg 840
cgcggcacaa gcggacctac cagccttaac acggtgcact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 358
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 358
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 359
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 359
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 360
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 360
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 361
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 361
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctata gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 362
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 362
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 363
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 363
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcaga atgggttaaa 780
atagttcaag gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 364
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 364
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Lys Ile Val Gln Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 365
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 365
```
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcaga atgggttaac 780
atatcgtgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 366
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 366
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 367
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 367
```
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatcc gcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 368
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 368
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Pro Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Thr Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 369
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 369
```
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaaa 780
catgttcaag gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgccg 840
cgcggcgtga gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 370
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 370
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 371
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 371
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgaaga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 372
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 372
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Met Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Glu
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 373
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 373
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagctggaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 374
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 374
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Trp Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 375
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 375
```
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattatagcg aggggattac gccatcagtc ggggcgcttg ctgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggttt gcctgtgctg 840
gctggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 376
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 376
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Ser Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Ala Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 377
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 377
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 378
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 378
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Met Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 379
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 379
```
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataatgct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcaga atgggttgac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtgc cgggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 380
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

Glu Ile Arg Ser Ala Val Glu
        355

<210> 381
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 381
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtagcat ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 382
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 382
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Ala Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 383
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 383
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa ccttctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
```

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 384
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 384
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 385
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 385
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatagaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 386
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 386
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

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Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Glu Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 387
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 387
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atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataaccct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattatagcg aggggattac gccatcagtc ggggcgcttg ctgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggttt gcctgtgctg 840
agaggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 388
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 388
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Ser Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Ala Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 389
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 389
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttacag gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacagtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 390
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 390
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160

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Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Thr Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 391
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 391
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttagtacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 392

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 392
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ser Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 393
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 393
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct ggttgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 394
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 394
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

```
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Val Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 395
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 395
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gcaatacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 396
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 396
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Asn Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 397
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 397
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 398
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 398
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 399
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 399
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 400
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

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

<210> 401
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 401
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacagtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtaggtt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcaga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 402
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 402
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Gly Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 403
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 403
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccgtaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 404
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 404
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Arg Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 405
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 405
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac catatcttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 406
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 406
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Tyr Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

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Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 407
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 407
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 408
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 408

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

<210> 409
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 409
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataatgct ggccatggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttgac 780
catgttgaag gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtgc cgggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 410
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 410

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asp His Val Glu Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Pro Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 411
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 411
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagataac atcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 412
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 412
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 413
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 413
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatata tgataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 414
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 414

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 415
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 415
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttcgt acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 416
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 416
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 417
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 417
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ttggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggaatggc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 418
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 418

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

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 419
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 419
```
atgatcgagt caaaaacata cgccgttttg ggactgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttg cggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcaga atgggttaac 780
cattcgtgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcacaa gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 420
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 420
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Leu Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 421
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 421
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac catgtcttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 422
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 422
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 423
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 423
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccca agccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 424
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 424
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 425
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 425
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttagt acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 426
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 426
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Ser Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 427
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 427
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttagg acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacctacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 428
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 428
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 429
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 429
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga tatgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
```

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 430
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 430
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 431
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 431
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtatgg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 432
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 432
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Met Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 433
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 433
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

catgtttgtg gccagacccc ggccacaatt tatgaagtta tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 434
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 434
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Val Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 435
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 435
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 436
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 436
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Val Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 437
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 437
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
agtggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 438
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 438
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 439
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 439
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctaggctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 440
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 440
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 441
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 441
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 442
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 442
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 443
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 443
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 444
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 444
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asp Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 445
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 445
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 446
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 446
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 447
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 447
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgttgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 448
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 448
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 449
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 449
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 450

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 450
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 451
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 451
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 452
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 452
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 453
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 453
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaaatta tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 454
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 454
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ile Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 455
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 455
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcagtga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 456
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 456
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 457
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 457
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc tggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctgttac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 458
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 458
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Leu Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Val Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 459
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 459
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 460
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 460
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 461
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 461
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
ccacaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaaacga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 462
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 462
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Thr Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 463
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 463
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggtatac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 464
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 464
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Tyr Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 465
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 465
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ttgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 466
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 466

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

<210> 467
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 467
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtcttg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 468
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 468
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Leu Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 469
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 469
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccacatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 470
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 470
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 471
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 471
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tggtataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 472
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 472

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 473
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 473
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaattct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 474
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 474
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 475
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 475
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 476
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 476

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

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 477
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 477
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac ccaattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 478
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 478
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 479
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 479
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

```
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg ggaagttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 480
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 480

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

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 481
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 481
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 482
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 482
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 483
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 483
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggtatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 484
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 484
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 485
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 485
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacttt gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 486
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 486
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 487
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 487
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

ttgtataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 488
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 488
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Leu Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 489
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 489
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggcccatatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 490
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 490
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala His Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 491
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 491
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgagtaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

```
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 492
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 492

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

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 493
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 493
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttatg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 494
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 494
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Tyr Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 495
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 495
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagc atcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 496
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 496
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Ala Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 497
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 497
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agggtgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 498
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 498
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Gly Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 499
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 499
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 500
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 500
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 501
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 501
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 502
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 502
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 503
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 503
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcaga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 504
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 504
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Trp Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 505
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 505
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtggaa 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 506
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 506
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160

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Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Glu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 507
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 507
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccacaact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 508

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 508
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Gln Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 509
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 509
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccttt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 510
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 510
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Leu Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 511
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 511
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacaatgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 512
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 512
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Asn Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 513
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 513
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttgatt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 514
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 514
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 515
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 515
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacacg caagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 516
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 516
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Ala Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 517
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 517
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagatta atgaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 518
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 518
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Asn Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 519
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 519
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttttg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 520
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 520
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Phe Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 521
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 521
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 522
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 522
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 523
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 523
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccaattgc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 524
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 524

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

<210> 525
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 525
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatg ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 526
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 526
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Val Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 527
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 527
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt tgataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 528
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 528
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 529
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 529
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 530
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 530

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 531
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 531
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agttggtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 532
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 532
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 533
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 533
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgctgtgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 534
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 534
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Cys Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 535
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 535
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 536
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 536
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 537
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 537
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 538
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 538
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Gly Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 539
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 539
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgctta tggagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 540
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 540
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 541
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 541
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
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cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaatcc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 542
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 542
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Asn Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 543
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 543
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 544
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 544
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 545
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 545
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 546
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 546
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Val Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 547
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 547
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggtgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcgg tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 548
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 548
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Val Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 549
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 549
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

```
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077


<210> 550
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 550
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
```

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 551
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 551
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 552
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 552
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 553
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 553
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtctgctggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggtgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 554
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 554
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Cys Trp Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 555
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 555
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acctgccggt ccgagagacc aggacaggtt acggtattct ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atggctgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcgg tgcagggtct gcctgtgctg 840
aggggctggt cgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 556
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 556
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Phe Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Leu Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Val Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 557
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 557
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtctgccggt ccgagagacc aggacaggtt acggtattct ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggtgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 558
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 558
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Phe Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 559
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 559
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgtc ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 560
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 560
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Val Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 561
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 561
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc tggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggatcac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 562
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 562
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Leu Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 563
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 563
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc tggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 564
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 564
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160

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Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Leu Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 565
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 565
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcattgcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 566

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 566
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ser
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 567
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 567
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtctgccggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atggatgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 568
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 568
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 569
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 569
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 570
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 570
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Val Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 571
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 571
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 572
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 572
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 573
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 573
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtctgccggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggtgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 574
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 574
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 575
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 575
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc tggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggatcac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 576
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 576
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Leu Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Val Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 577
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 577
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 578
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 578
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 579
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 579
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 580
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 580
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 581
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 581
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
accgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctggc acggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 582
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 582

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

<210> 583
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 583
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 584
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 584

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 585
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 585
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tgtcgctggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atggctgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 586
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 586
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 587
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 587
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 588
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 588

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 589
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 589
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
accgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 590
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 590
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 591
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 591
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 592
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 592
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Val Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 593
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 593
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 594
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 594
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 595
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 595
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 596
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 596
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Val Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Trp Pro Thr Ser
275 280 285

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 597
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 597
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 598
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 598
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 599
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 599
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 600
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 600
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 601
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 601
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 602
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 602
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 603
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 603
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 604
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 604
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 605
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 605
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcattgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 606
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 606
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 607
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 607
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
accgcttggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atggctgaac 780
```

```
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077


<210> 608
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 608
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Ala Trp Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Leu Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
```

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 609
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 609
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttacg agtctggtac cccgttccat 660
tactataccg aggggatcac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgtc ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 610
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 610
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Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Tyr Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Val Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 611
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 611
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 612
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 612
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 613
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 613
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 614
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 614
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 615
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 615
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcattgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggcgtca gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 616
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 616
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 617
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 617
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 618
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 618
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 619
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 619
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 620
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 620
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 621
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 621
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 622
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 622
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 623
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 623
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 624

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 624
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 625
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 625
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acctgctggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctggc acggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 626
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 626
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Trp Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 627
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 627
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgcg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcattgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggcgtca gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 628
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 628
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 629
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 629
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgcg agtctgttac ccagttccat 660
tactataccg aggggtatac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggcgtca gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 630
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 630
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 631
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 631
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 632
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 632
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Val Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 633
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 633
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 634
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 634
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 635
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 635
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
accgcttggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atggatgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcgg tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 636
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 636
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Ala Trp Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Met Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Val Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 637
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 637
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 638
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 638
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 639
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 639
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
acatgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggcgtca gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 640
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 640

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

<210> 641
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 641
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 642
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 642
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 643
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 643
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggtatac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 644
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 644
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 645
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 645
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcattgcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 646
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 646

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 647
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 647
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgcg agtctggtac cccgttccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 648
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 648
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 649
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 649
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgtc ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 650
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 650

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

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 651
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 651
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaaatca tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 652
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 652
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 653
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 653
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 654
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 654
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Val Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 655
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 655
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagtga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 656
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 656
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 657
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 657
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagtga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 658
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 658
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Val Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 659
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 659
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 660
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 660
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 661
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 661
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
```

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagtga tgcagggtct gcctgtcctg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 662
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 662
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Val Met Gln Gly Leu Pro Val Leu Ser Gly Val Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 663
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 663
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtctcg agtctggtac cccgttccat 660
ttgtataccg aggggatcac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgtc ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 664
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 664
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Leu Glu Ser Gly Thr Pro Phe His Leu Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Trp Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 665
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 665
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 666
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 666
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Val Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 667
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 667
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtatgg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 668
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 668
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Met Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 669
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 669
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 670
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 670
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Ser Trp Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 671
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 671
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 672
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 672
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 673
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 673
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 674
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 674
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 675
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 675
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 676
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 676
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 677
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 677
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaaatca tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 678
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 678
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ile Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 679
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 679
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catatcttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatata tgataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggcgtga gcggacctac cagctggaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 680
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 680
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Tyr Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Met Ile Thr Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Trp Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 681
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 681
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 682

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 682
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 683
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 683
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatata tgatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gcaacacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 684
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 684
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Met Met Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175

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

<210> 685
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 685
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 686
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 686
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 687
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 687
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatata tgatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 688
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 688
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Met Met Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 689
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 689
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 690
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 690
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 691
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 691
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtattct ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
cttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atggatgaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcgg tgcagggtct gcctgtgctg 840
gcgggctggc acggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 692
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 692
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Phe Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Leu His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Met Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Val Gln Gly Leu Pro Val Leu Ala Gly Trp His Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 693
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 693
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgtatgg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagtga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 694
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 694
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Met Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Val Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 695
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 695
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatata tgataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttaccg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 696
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 696
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Met Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Thr Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 697
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 697
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 698
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 698

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

<210> 699
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 699
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 700
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 700
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 701
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 701
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtctcg agtctggtac cccgttccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 702
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 702
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 703
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 703
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtatgg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 704
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 704

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 705
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 705
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 706
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 706
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 707
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 707
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 708
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 708
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 709
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 709
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 710
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 710
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 711
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 711
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

```
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 712
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 712

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

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 713
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 713
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 714
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 714
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 715
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 715
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 716
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 716
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Met Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 717
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 717
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggtatac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 718
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 718
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 719
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 719
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gcaacacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 720
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 720
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Met Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Asn Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 721
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 721
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagtga tgcagggtct gcctgtcctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 722
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 722
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Val Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 723
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 723
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

```
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077


<210> 724
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 724
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
```

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 725
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 725
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 726
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 726
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 727
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 727
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 728
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 728
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Met Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 729
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 729
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagctggaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 730
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 730
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Trp Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 731
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 731
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggtcctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gcaacacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 732
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 732
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Asn Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 733
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 733
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 734
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 734
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 735
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 735
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 736
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 736
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 737
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 737
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 738
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 738
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 739
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 739
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 740

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 740
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 741
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 741
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 742
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 742
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 743
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 743
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 744
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 744
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 745
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 745
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgtc ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 746
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 746
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 747
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 747
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 748
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 748
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 749
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 749
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 750
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 750
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 751
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 751
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 752
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 752
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 753
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 753
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 754
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 754
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 755
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 755
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 756
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 756

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

<210> 757
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 757
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgtatgg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 758
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 758

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 759
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 759
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catatcttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 760
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 760
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 761
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 761
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 762
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 762

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 763
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 763
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 764
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 764
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 765
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 765
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcattgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgtc ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 766
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 766
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Ser Trp Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 767
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 767
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 768
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 768
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 769
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 769
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccagttct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 770
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 770
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Val Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Val Ser Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 771
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 771
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttaccg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 772
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 772
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 773
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 773
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 774
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 774
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 775
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 775
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 776
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 776
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 777
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 777
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660

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tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 778
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 778

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

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 779
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 779
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagtga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 780
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 780
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Val Met Gln Gly Leu Pro Arg Leu Ser Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 781
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 781
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgcg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

```
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttcgt acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 782
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 782

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

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 783
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 783
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttcgt acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 784
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 784
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Arg Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 785
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 785
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttaccg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 786
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 786
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Thr Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 787
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 787
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gcaacacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 788
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 788
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Asn Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 789
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 789
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
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ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 790
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 790
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 791
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 791
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 792
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 792
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 793
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 793
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catatcttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 794
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 794
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Tyr Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Met Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 795
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 795
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 796
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 796
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 797
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 797
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 798

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 798
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 799
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 799
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttcgt acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 800
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 800
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175

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

<210> 801
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 801
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 802
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 802
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 803
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 803
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gcaacacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 804
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 804
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Met Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 805
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 805
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgtatgg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 806
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 806
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Met Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Val Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 807
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 807
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 808
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 808
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 809
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 809
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 810
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 810
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 811
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 811
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 812
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 812
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 813
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 813
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctgtcctg 840
cgcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 814
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 814

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

<210> 815
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 815
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaat acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggaccgacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 816
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 816

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Pro Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 817
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 817
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 818
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 818
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 819
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 819
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 820
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 820

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 821
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 821
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc tggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggatcac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtctcgga gtgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gcgggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 822
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 822
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 823
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 823
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggcgtta gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 824
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 824

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

```
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Val Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 825
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 825
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggctgga gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 826
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 826
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 827
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 827
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagctggaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 828
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 828
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
275 280 285

```
Trp Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 829
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 829
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacagcgg agccatcata gcggaaggac catgccttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttatgacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccatgg aacagatagg gtcggtcctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 830
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 830
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Ser Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Cys Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 831
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 831
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaacct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
cgcacctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 832
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 832
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Thr Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 833
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 833
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccattgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc cgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 834
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 834
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 835
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 835
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc tggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
```

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcgttgcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
cgcggcgtca gctggcctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 836
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 836
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Leu Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Val Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Val Ser Trp Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 837
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 837
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attgtggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaactct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccgt tgccacaatt tatgaagcga tgcagggtct gcctagactg 840
agcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 838
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 838
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Phe Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Val Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Met Leu Phe Trp Cys Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Val Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Arg Leu Ser Gly Trp Ser Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 839
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 839
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attacggtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tggtgccgct ccgagagacc aggacaggtt acggtatatt ttataacact ggccgaagac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

catgtttgtg gccagacccc ggccacaatt tatgaagtga tgcagggtct gcctagactg 840
cgcggctgga gcggacctac cagccttaac acggaacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 840
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 840
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Trp Cys Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Glu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Val Met Gln Gly Leu Pro Arg Leu Arg Gly Trp Ser Gly Pro Thr Ser
275 280 285
Leu Asn Thr Glu His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 841
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 841
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgggtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 842
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 842
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Gly Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 843
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 843
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgggtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 844
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 844
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Gly Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 845
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 845
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tggatacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 846
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 846
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Asp Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 847
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 847
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tggcaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
```

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 848
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 848
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ala Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 849
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 849
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tggcaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 850
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 850
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ala Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 851
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 851
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 852
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 852
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 853
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 853
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgggtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 854
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 854
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Gly Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 855
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 855
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgaatacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 856

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 856
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Asn Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 857
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 857
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgcttacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 858
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 858
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 859
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 859
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgttgacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 860
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 860
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Leu Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 861
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 861
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgttgacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 862
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 862
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 863
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 863
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 864
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 864
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 865
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 865
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgagcaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 866
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 866
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Ser Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 867
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 867
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 868
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 868
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 869
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 869
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
gcacacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 870
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 870
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ala His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 871
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 871
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 872
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 872

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

<210> 873
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 873
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggccttggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 874
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 874
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Leu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 875
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 875
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac cgggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg ggaagttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 876
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 876
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 877
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 877
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
agtgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 878
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 878
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 879
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 879
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
tttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 880
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 880
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 881
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 881
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 882
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 882
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 883
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 883
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc tttttacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 884
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 884
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 885
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 885
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 886
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 886
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 887
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 887
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 888
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 888
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 889
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 889
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 890
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 890
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 891
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 891
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggccttggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 892
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 892
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 893
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 893
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
tgtcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
```

```
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 894
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 894

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

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 895
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 895
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 896
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 896
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 897
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 897
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccttgac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
```

catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 898
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 898
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Leu Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 899
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 899
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 900
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 900
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Met Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 901
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 901
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggcccatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 902
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 902
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Gly Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala His Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 903
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 903
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 904
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 904
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 905
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 905
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagatta atgaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
```

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 906
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 906
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Asn Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Glu Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 907
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 907
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 908
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 908
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 909
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 909
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 910
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 910
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 911
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 911
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagcctttat acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 912
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 912
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Tyr Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 913
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 913
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtattgt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 914

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 914
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val Leu Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 915
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 915
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacggtc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 916
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 916
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 917
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 917
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
agtgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 918
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 918
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 919
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 919
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgagcaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 920
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 920
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 921
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 921
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatagcact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 922
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 922
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Ala Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 923
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 923
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agggtgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 924
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 924
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Gly Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 925
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 925
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgagcaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 926
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 926
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Ser Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 927
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 927
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 928
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 928
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 929
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 929
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 930
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 930

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

<210> 931
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 931
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 932
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 932
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 933
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 933
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagatta atgaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 934
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 934
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 935
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 935
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaaccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 936
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 936

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

```
Glu Trp Val Asn His Val Cys Gly Gln Asn Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 937
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 937
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtaatgt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 938
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 938
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 939
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 939
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300

```
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 940
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 940

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

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 941
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 941
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 942
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 942
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 943
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 943
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

```
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agggtgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 944
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 944

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

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 945
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 945
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 946
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 946
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 947
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 947
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 948
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 948
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 949
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 949
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagcttat 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtat gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 950
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 950
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 951
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 951
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 952
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 952
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 953
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 953
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaaaga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 954
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 954
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Lys
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 955
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 955
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
```

catgtttgtg gccagaaccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 956
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 956
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Ser Trp Val Asn His Val Cys Gly Gln Asn Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 957
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 957
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
tttcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 958
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 958
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Phe His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 959
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 959
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 960
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 960
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Gly Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Glu Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 961
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 961
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 962
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 962
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 963
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 963
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgcgtaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 964
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 964
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Arg Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 965
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 965
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agggtgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 966
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 966
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Gly Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 967
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 967
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacaatgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatcatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
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<210> 968
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 968
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Asn Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn His Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 969
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 969
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 970
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 970
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160

```
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 971
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 971
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcgg ttcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 972

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 972
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Val Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 973
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 973
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagatta atgaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agggtgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggcccatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 974
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 974
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Asn Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 975
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 975
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac gcagtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 976
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 976
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Ala Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 977
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 977
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga ttggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 978
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 978
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 979
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 979
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacaatgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatcatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 980
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 980
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Asn Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Gly Lys Ile Ala
                85   90   95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn His Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 981
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 981
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaccaa agccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 982
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 982
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Lys Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 983
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 983
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 984
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 984
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Glu Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 985
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 985
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagaaccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 986
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 986
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Asn Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 987
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 987
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaatga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 988
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 988

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

<210> 989
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 989
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggtga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 990
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 990
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 991
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 991
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacaatgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agttggtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatcatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 992
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 992
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 993
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 993
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
atgcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 994
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 994

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

```
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 995
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 995
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggccattgac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 996
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 996
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 997
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 997
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttgcatttcc 300

gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agggtgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggaccatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 998
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 998
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Gly Lys Ile Ala
85 90 95
Ser Cys Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Gly Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asp His Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 999
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 999
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggcccatatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1000
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1000
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 1001
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1001
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420

gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
atttataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1002
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1002
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Ile Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1003
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1003
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1004
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1004
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 1005
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1005
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatagcact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1006
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1006
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Ala Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 1007
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1007
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagaaccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1008
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1008
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 1009
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1009
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggacaatgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaggta aaatcgccag ttggatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1010
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1010
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Asn Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Gly Lys Ile Ala
85 90 95
Ser Trp Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1011
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1011
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1012
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1012
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1013
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1013
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgttgtg aggaaggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta gaagttccgt cggtcgcgga atgggttaac 780
```

```
catgtttgtg gccagacccc gaatacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077


<210> 1014
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1014
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Glu Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Glu Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Asn Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
```

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1015
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1015
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg aggcatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
accgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgag ctgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1016
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1016
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Gly
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Ser Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1017
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1017
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
accgctcggt ccgagagacc aggacaggtt acggtagagt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgccactgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagaaccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1018
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1018
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Thr Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Glu Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Pro Leu Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Asn Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 1019
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1019
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 1020
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1020
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser

```
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gly Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1021
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1021
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1022
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1022
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1023
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1023
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttatagctct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
atccacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1024
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1024
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Ala Leu Ala Gln Asp

```
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1025
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1025
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgaccaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtattct tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1026
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1026
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1027

<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1027
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataactct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1028
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1028
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile

```
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1029
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1029
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
atgcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1030
<211> 359

<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1030
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Met His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1031
<211> 1077
<212> DNA

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1031
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1032
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1032
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr

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

<210> 1033
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1033
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaaccctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1034
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1034
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1035
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1035
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
atgcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1036
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1036
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Met His Pro Leu Thr Asn Leu Leu

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

<210> 1037
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1037
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1038
<211> 359
<212> PRT
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1038
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1039
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1039
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
atccacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1040
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1040
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu

```
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1041
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1041
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1042
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1042
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1043
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1043

atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1044
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1044
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu

```
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1045
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1045
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1046
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1046
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
```

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

<210> 1047
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1047
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120

```
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1048
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1048

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

```
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1049
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1049
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1050
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1050
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
```

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

<210> 1051
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1051
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240

attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1052
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1052
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu

```
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1053
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1053
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1054
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1054
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
```

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

<210> 1055
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1055
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360

atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacgggc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1056
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1056
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Gly Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser

```
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1057
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1057
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaagga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1058
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1058
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
```

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

<210> 1059
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1059
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
```

tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1060
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1060
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Met Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro

```
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1061
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1061
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggccgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1062
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1062
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
```

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

<210> 1063
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1063
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600

attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaatga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1064
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1064
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Asn
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp

```
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1065
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1065
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaatga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1066
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1066
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
```

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

<210> 1067
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1067
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720

```
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtaatgt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077


<210> 1068
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1068
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Met Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
```

```
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1069
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1069
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1070
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1070
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
```

```
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1071
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1071
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
```

aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1072
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1072
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Met Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala

```
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1073
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1073
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
atctataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1074
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1074
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
```

```
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Ile Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1075
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1075
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
agcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggccgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
```

gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1076
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1076
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu

355

<210> 1077
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1077
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactatgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcggaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1078
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1078
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser

```
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Met Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Gly Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1079
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1079
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggccgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtactg 840
aggggctgga tgggacctac cagccttaac acggtaatgt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1080
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1080
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Met Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1081
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1081
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgccaacact gttaaacgct gctcgtgttg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaatga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaat gccgtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1082
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1082
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp

```
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Pro Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Val Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Asn
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Ala Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1083
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1083
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta atggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttctgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggccgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtattct tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1084
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1084
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Met Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Leu Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1085

<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1085
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgaagctgta 600
attcacccgc tgactacact gttaaacgct gctcgtgttg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtatact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1086
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1086
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile

```
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Val Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Tyr Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1087
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1087
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1088
<211> 359

<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1088
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1089
<211> 1077
<212> DNA

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1089
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1090
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1090
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr

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

<210> 1091
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1091
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaaccctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1092
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1092
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1093
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1093
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgaagctgta 600
attcacccgc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaat gccgtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1094
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1094
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu

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

<210> 1095
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1095
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
gctcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1096
<211> 359
<212> PRT
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1096
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gly Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ala His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1097
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1097
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataactct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
gctcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1098
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1098
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ala His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu

```
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1099
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1099
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataactct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
atgcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1100
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1100
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Met His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1101
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1101

atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1102
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1102
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu

```
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1103
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1103

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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacgggc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1104
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1104

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Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
```

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

<210> 1105
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1105
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120

aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1106
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1106
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Ser Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala

```
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1107
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1107
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
tcggctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgaagctgta 600
attcacccgc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttcagg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1108
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1108
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
```

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

<210> 1109
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1109
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240

attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatagctct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1110
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1110
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Ala Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu

```
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1111
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1111
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacaact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1112
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1112
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
```

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

<210> 1113
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1113
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360

```
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1114
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1114

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

```
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1115
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1115
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatagctct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1116
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1116
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
```

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

<210> 1117
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1117
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatagctct ggcccaggac 480
```

```
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1118
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1118

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

```
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1119
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1119
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgtg 600
gctcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1120
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1120
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
```

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

<210> 1121
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1121
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
```

attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1122
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1122
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp

```
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1123
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1123
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1124
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1124
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
```

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

<210> 1125
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1125
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacgct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720

cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1126
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1126
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys

```
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1127
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1127
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1128
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1128
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
```

```
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gly Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1129
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1129
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataactct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
```

aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1130
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1130
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala

```
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1131
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1131
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1132
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1132
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
```

```
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1133
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1133
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
```

gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1134
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1134
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu

355

<210> 1135
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1135
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1136
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1136
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser

```
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gly Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1137
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1137
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataactct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagttgta 600
attcacccgc tgactacgct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgatt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1138
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1138
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Val Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1139
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1139
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1140
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1140
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp

```
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1141
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1141
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataactct ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
gaggtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1142
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1142
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1143

<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1143
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttgagg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1144
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1144
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile

```
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Glu Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1145
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1145
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1146
<211> 359

<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1146
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1147
<211> 1077
<212> DNA

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1147
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaat gccgtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1148
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1148
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr

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

<210> 1149
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1149
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaaccctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaat gccgtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1150
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1150
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245   250   255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Ala Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1151
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1151
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaagctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1152
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1152
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu

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

<210> 1153
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1153
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1154
<211> 359
<212> PRT
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1154
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1155
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1155
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1156
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1156
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu

```
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1157
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1157
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1158
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1158
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1159
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1159

atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgtgctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1160
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1160
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu

```
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1161
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1161
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaagga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1162
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1162
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
```

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

<210> 1163
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1163
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120

```
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgtgttg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcttgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1164
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1164

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

```
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Val Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1165
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1165
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1166
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1166
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
```

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

<210> 1167
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1167
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240

attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcttgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1168
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1168
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Leu
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu

```
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1169
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1169
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcaccctc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcttgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1170
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1170
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
```

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

<210> 1171
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1171
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360

```
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
atgtataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgttgagg gccagacccc ggccacaatt tatgaagcgg tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1172
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1172

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

```
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1173
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1173
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1174
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1174
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
```

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

<210> 1175
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1175
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480

tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1176
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1176
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro

```
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1177
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1177
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcaatga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1178
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1178
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
```

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

<210> 1179
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1179
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600

attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1180
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1180
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp

```
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1181
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1181
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgcagaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcttgga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1182
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1182
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
```

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

<210> 1183
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1183
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat tgaagctgta 600
attcacccgc tgagtacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaagaa 720

cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgccga atgggttaac 780
catgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1184
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1184
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Ser Thr Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
245 250 255
Glu Trp Val Asn His Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys

```
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1185
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1185
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct taaccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataacact ggcccaggac 480
tttgcatgtc tcccagcggc aaaggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacgggc tgactacact gttaaacgct gctcgttgtg agtctggtac cccattccat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggacgctgaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcgcgga atgggttaac 780
catgtttgcg gccagccccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacact tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactgata gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1186
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1186
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Asn Pro Gly Ala Thr
```

```
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Thr Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Lys Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Gly Leu Thr Thr Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe His Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Ala Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Ala
                245                 250                 255
Glu Trp Val Asn His Val Cys Gly Gln Pro Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Ile Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1187
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1187
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840

aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1188
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1188
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala

```
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1189
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1189
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatac cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctcgtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtaatgt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 1190
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1190
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
```

```
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Thr Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Arg Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Met Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1191
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1191
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa catgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttataggtct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agctggtcga aaacgtgttg catacttcgc tgactaatac cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtaatgt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
```

gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1192
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1192
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Met Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gly Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Leu Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Thr Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Met Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu

355

<210> 1193
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1193
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctcgtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacatt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1194
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1194
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser

```
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Arg Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val His Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1195
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1195
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctagcac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gcctgaactg 840
aggggctgga tgggacctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1196
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1196
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Ser Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Glu Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1197
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1197
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatagcgct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc agctggtcga aaacgtgttg catacttcgc tgactaatat cgaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1198
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1198
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Ala Leu Ala Gln Asp

```
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Leu Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Ile Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1199
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1199
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa gcgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cggtctcttt 420
gtagctaaat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtattct tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1200

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1200
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Ser Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1201
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1201
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaacca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cggtctcttt 420
gtagctaaat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaattt agaagctgta 600
atacacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcaa atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtattct tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1202
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1202
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Thr Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 1203
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1203
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa gcgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaacca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga cttactcttt 420
gtagctaaat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaattt agaagctgta 600
atacacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1204
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1204
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Ser Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Thr Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Leu Leu Phe Val Ala Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1205
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1205
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gaagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1206
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1206
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Glu Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 1207
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1207
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaacca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1208
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1208
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Thr Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275   280   285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1209
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1209
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga cttactcttt 420
gaagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggtcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1210
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1210
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Leu Leu Phe Glu Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205

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Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1211
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1211
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cttactcttt 420
gaagctaaat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1212
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1212
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Glu Ala Lys Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275   280   285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1213
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1213
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga cttactcttt 420
gaagctaaat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1214
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1214
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Leu Leu Phe Glu Ala Lys Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1215
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1215
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
ggtcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1216
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1216

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

<210> 1217
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1217
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga tctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1218
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1218
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asp Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1219
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1219
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1220
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1220
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 1221
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1221
atgatcgagt caaaaacata cgccgttttg ggaatgggaa gcgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cggtctcttt 420
gtagctagat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
atacacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtattct tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1222
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1222

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

```
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1223
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1223
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa ctttctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1224
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1224
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 1225
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1225
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300

```
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cggtctcttt 420
gtagctagat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtattct tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1226
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1226

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

```
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1227
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1227
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaga cttactcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
ggccacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggtcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1228
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1228
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 1229
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1229
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cggtctcttt 420
```

gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1230
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1230
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285

```
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1231
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1231
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cggtctcttt 420
gtagctaaat ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtacaat tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1232
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1232
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 1233
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1233
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcaacaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1234
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1234
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Thr Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Leu Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Gly Pro Thr Ser
275 280 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 1235
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1235
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcaa aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cctgctcttt 420
gtcgctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tgggacctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1236
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1236
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 1237
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1237
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1238
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1238
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
275 280 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1239
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1239
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1240
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1240
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
```

```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1241
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1241
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
```

gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1242
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1242
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Lys Ser
275 280 285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1243
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1243
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1244
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1244
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100                 105                 110
```

```
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Ile Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1245
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1245
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtacagt tcagcaacga tgtaagcacc 900
```

ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1246
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1246
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Lys Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350

Glu Ile Arg Ser Ala Val Glu
        355

<210> 1247
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1247
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag   1077

<210> 1248
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1248
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125

```
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Lys Ser
        275                 280                 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1249
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1249
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgta gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
```

ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1250
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1250
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Glu Val Cys Ser Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
275 280 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1251
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1251
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1252
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1252
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140

```
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1253
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1253
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1254
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1254
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Gly Ser
        275   280   285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1255
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1255
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1256
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1256
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160

```
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1257
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1257
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1258

<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1258
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Gly Ser
275 280 285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
340 345 350
Glu Ile Arg Ser Ala Val Glu
355

<210> 1259
<211> 1077

<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1259
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
atggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1260
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1260
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175

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

<210> 1261
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1261
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1262
<211> 359
<212> PRT

<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1262
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275   280   285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1263
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1263
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagatgc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1264
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1264
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Met Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190

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

<210> 1265
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1265
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1266
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1266
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Ala Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Ile Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Gly Ser
        275   280   285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1267
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1267
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gacagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1268
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1268
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205

```
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Ile Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1269
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1269
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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1270
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1270
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1   5   10   15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20   25   30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35   40   45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50   55   60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65   70   75   80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85   90   95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100   105   110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115   120   125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130   135   140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145   150   155   160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165   170   175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180   185   190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195   200   205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210   215   220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225   230   235   240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245   250   255
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260   265   270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Lys Ser
        275   280   285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290   295   300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305   310   315   320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325   330   335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340   345   350
Glu Ile Arg Ser Ala Val Glu
        355

<210> 1271
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1271
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1272
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1272
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220

```
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1273
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1273

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atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1274
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1274

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

<210> 1275
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1275
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60

```
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1276
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1276

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

```
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1277
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1277
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1278
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1278
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
```

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

<210> 1279
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1279
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180

```
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1280
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1280

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

```
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Gly Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1281
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1281
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1282
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1282
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
```

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

<210> 1283
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1283
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300

gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1284
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1284
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270

```
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Gly Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1285
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1285
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1286
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1286
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Ala Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
```

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

<210> 1287
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1287
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420

gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1288
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1288
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Val Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
275 280 285

```
Leu Asn Thr Val Gln Phe Lys Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1289
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1289
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagaaaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1290
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1290
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
```

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

<210> 1291
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1291
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggctgcgg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
```

cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctaa aagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1292
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1292
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Ala Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Lys Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300

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

<210> 1293
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1293
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctgg cagccttaac acggtacagt tcaaaaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag    1077
```

<210> 1294
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1294
```
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1               5                   10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
```

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

<210> 1295
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1295
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
gcctatttag cattgaaggg ccagcgtgta ctggcttggg acatcgatgc tcagagaatc 120
aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
```

tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtatttt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1296
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1296
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
275 280 285
Leu Asn Thr Val Phe Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320

```
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```

<210> 1297
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1297
```
atgatcgagt caaaaacata cgccgttttg ggaatgggaa acgggggtca cgcatttgcc 60
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aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atgggttaac 780
gatgtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
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ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
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<210> 1298
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1298
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1               5                  10                  15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
            20                  25                  30
Ala Asp Ile Asp Ala Gln Arg Ile Lys Glu Ile Gln Asp Arg Gly Ala
        35                  40                  45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
    50                  55                  60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65                  70                  75                  80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
                85                  90                  95
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```
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
            100                 105                 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
        115                 120                 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
    130                 135                 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145                 150                 155                 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
                165                 170                 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
            180                 185                 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
        195                 200                 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
    210                 215                 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225                 230                 235                 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
                245                 250                 255
Glu Trp Val Asn Asp Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
            260                 265                 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Lys Ser
        275                 280                 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
    290                 295                 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305                 310                 315                 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
                325                 330                 335
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
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<210> 1299
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1299
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aaagagattc aggaccgtgg agccatcata gcggaaggac caggacttgc tgggactgct 180
cacccggatc ttgtgacctc agatataggt ttggcggtta aagacgctga tgtgatactg 240
attaccgtgc cggccatcca ccacgcttcc attgcagcca aaatcgccag ttacatttcc 300
gagggtcagt tgattatcct tagccctggg gcgacgggtg gagcgctgga attccggaaa 360
atcctgcgtg aaaatggtgc gccggaggta acgatcgggg aaacctcaaa cgggctcttt 420
gtagctcggt ccgagagacc aggacaggtt acggtatatt ttatacagct ggcccaggac 480
tttgcatgtc tcccagcggc aatggctgga tgggccctgg aacagatagg gtcggttctt 540
cctcaatacc aggctgtcga aaacgtgttg catacttcgc tgactaatct ggaagctgta 600
attcacccgc tgactaatct gttaaacgct gctcgttgtg agtctggtac cccattcgat 660
tattataccg aggggattac gccatcagtc ggggcgcttt gcgagaaagt ggaccaggaa 720
cgcatagcaa tcgcaaaggc tttcgattta aacgttccgt cggtcggcga atggattaac 780
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gaagtttgtg gccagacccc ggccacaatt tatgaagcga tgcagggtct gccttttctg 840
aggggctgga tggttcctac cagccttaac acggtacagt tcagcaacga tgtaagcacc 900
ggactggtac cgttatccga actgggtcgg gtggtgaatg tgcctacccc acttatcgat 960
gctgttcttc tgttgatcag tgaactggtt gacgtggatt tcagaaagga aggtcgtacc 1020
ttggaaaaat taggtctgag cggacttacc gccgcggaaa taagaagtgc tgttgag 1077

<210> 1300
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Opine dehydrogease Variant from Arthrobactor sp. strain 1C

<400> 1300
Met Ile Glu Ser Lys Thr Tyr Ala Val Leu Gly Met Gly Asn Gly Gly
1 5 10 15
His Ala Phe Ala Ala Tyr Leu Ala Leu Lys Gly Gln Arg Val Leu Ala
20 25 30
Trp Asp Ile Asp Ala Gln Lys Ile Lys Glu Ile Gln Asp Arg Gly Ala
35 40 45
Ile Ile Ala Glu Gly Pro Gly Leu Ala Gly Thr Ala His Pro Asp Leu
50 55 60
Val Thr Ser Asp Ile Gly Leu Ala Val Lys Asp Ala Asp Val Ile Leu
65 70 75 80
Ile Thr Val Pro Ala Ile His His Ala Ser Ile Ala Ala Lys Ile Ala
85 90 95
Ser Tyr Ile Ser Glu Gly Gln Leu Ile Ile Leu Ser Pro Gly Ala Thr
100 105 110
Gly Gly Ala Leu Glu Phe Arg Lys Ile Leu Arg Glu Asn Gly Ala Pro
115 120 125
Glu Val Thr Ile Gly Glu Thr Ser Asn Gly Leu Phe Val Ala Arg Ser
130 135 140
Glu Arg Pro Gly Gln Val Thr Val Tyr Phe Ile Gln Leu Ala Gln Asp
145 150 155 160
Phe Ala Cys Leu Pro Ala Ala Met Ala Gly Trp Ala Leu Glu Gln Ile
165 170 175
Gly Ser Val Leu Pro Gln Tyr Gln Ala Val Glu Asn Val Leu His Thr
180 185 190
Ser Leu Thr Asn Leu Glu Ala Val Ile His Pro Leu Thr Asn Leu Leu
195 200 205
Asn Ala Ala Arg Cys Glu Ser Gly Thr Pro Phe Asp Tyr Tyr Thr Glu
210 215 220
Gly Ile Thr Pro Ser Val Gly Ala Leu Cys Glu Lys Val Asp Gln Glu
225 230 235 240
Arg Ile Ala Ile Ala Lys Ala Phe Asp Leu Asn Val Pro Ser Val Gly
245 250 255
Glu Trp Ile Asn Glu Val Cys Gly Gln Thr Pro Ala Thr Ile Tyr Glu
260 265 270
Ala Met Gln Gly Leu Pro Phe Leu Arg Gly Trp Met Val Pro Thr Ser
275 280 285
Leu Asn Thr Val Gln Phe Ser Asn Asp Val Ser Thr Gly Leu Val Pro
290 295 300
Leu Ser Glu Leu Gly Arg Val Val Asn Val Pro Thr Pro Leu Ile Asp
305 310 315 320
Ala Val Leu Leu Leu Ile Ser Glu Leu Val Asp Val Asp Phe Arg Lys
325 330 335

```
Glu Gly Arg Thr Leu Glu Lys Leu Gly Leu Ser Gly Leu Thr Ala Ala
            340                 345                 350
Glu Ile Arg Ser Ala Val Glu
        355
```