SEQUENCE LISTING

<110> CODEXIS, INC.

<120> ENGINEERED TRANSAMINASE POLYPEPTIDES

<130> CX2-183WO1

<140>
<141> 2020-01-13

<150> US 62/792,518
<151> 2019-01-15

<160> 846

<210> 1
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 1
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attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 2
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 2
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 3
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 3

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attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 4
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 4
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125

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Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 5
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 5
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
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gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 6
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 6

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

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 7
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 7
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
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gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 8
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 8
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro

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        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 9
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc tacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
accccggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
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gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 10
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 11
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 11
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attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacaat 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
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gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctaacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 12
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 12
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Asn Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asn Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 13
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 13
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgagtttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 14
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 14
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ser Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 15
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 15
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gcttcgccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
```

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 16
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 16
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Ser
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 17
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 17
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggact ctgttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 18
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 18

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

<210> 19
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 19
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccggctgt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 20
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 21
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 21
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actggctgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 22
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 22
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Ala Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 23
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 23
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggggttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 24
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 24
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Gly Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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


<210> 25
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 25
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
```

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtaatcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 26
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 26
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Asn Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 27
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 27
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg ttgctggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 28
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 29

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 29
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 30
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 31
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 31
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggaca ttgttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 32
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 32
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Ile Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 33
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 33
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacattgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 34
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 34
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Ile
1               5                   10                  15
```

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

<210> 35
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 35
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccatctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 36
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 36
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe His Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 37
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 37
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctgct gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 38
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 38
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Ala Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

```
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330


<210> 39
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 39
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctacc ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttt gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 40
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 41
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 41
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggaccat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 42
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 42
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp His Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 43
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 43
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actgaagccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 44
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

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

<210> 45
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 45
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 46
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 47
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 47
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt ctccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 48
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 49
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 49
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tatggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 50
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 50
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 51
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 51
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgattgt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 52
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 52
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Ile Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 53
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 53
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacatgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 54

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 54
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Met Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 55
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 55
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 56
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 56
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Ser Ile Arg Leu

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

<210> 57
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 57
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacttgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
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gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 58
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 58
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

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

<210> 59
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 59
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacacg 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 60
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 61
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 61
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctg gtccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 62
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 62
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Gly Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 63
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 63
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgtttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
```

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 64
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 64
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Phe Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 65
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 65
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgaagttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 66
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 66
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 67
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 67
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accactcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 68
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 68
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Thr His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 69
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 69
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaaccga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 70
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 71
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 71
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgctatg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 72
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 72
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Met Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 73
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 73
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actgggagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 74
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 75
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 75
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggcg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 76
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 76
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
```

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

<210> 77
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 77
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgcgatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 78
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 78
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Ala Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160

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

<210> 79
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 79
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 80
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 81
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 81
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctcttccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 82
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 82
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Leu
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
```

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

<210> 83
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 83
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctcttgt gcggaatcta ttcgtttgat cccgccgctg 300
```

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 84
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 84
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Cys Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 85
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 85
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg acgctggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 86
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 86
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Thr Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 87
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 87
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
gggccgcaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 88
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 89
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 89
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggacgat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
```

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 90
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 91
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 91
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggtta ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 92
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 92
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 93
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 93

atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttctgtcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 94
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 94
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Cys Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

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

<210> 95
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 95
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aagggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 96
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 96
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Lys Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 97
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 97
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctacg atgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 98
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 98
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Asp Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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

<210> 99
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 99
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
cttcaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
```

accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 100
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 101
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 101
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttggttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 102
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 103
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 103
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcgacg gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 104
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 105
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 105
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctacg gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
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tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 106
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 107
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 107
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 108
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 108
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 109
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 109
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tgggtggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 110
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 111
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 111
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 112
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 112
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 113
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 113
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtat 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 114
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 114
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 115
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 115
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcatgt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
```

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 116
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 116
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro His Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 117
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 117
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atctggtact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 118
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 118

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

<210> 119
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 119
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttccgttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 120
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 121
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 121
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tgggggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gatggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 122
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 122
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Gly Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Asp Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 123
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 123
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acactaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 124
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 124
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Thr Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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


<210> 125
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 125
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
```

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga tctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 126
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 126
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Asp Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 127
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 127
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat catgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 128
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 128
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Met Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 129

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 129
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atccattact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 130
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 131
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 131
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagtttctga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 132
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 133
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 133
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctggaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 134
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 134
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 135
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 135
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctcttcg gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 136
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 136
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Ser Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 137
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 137
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacccatt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 138
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 138
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr His Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

```
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330


<210> 139
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 139
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccttaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 140
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 140
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
```

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

<210> 141
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 141
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttacgttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 142
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 142
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Thr Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 143
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 143
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
gggactcaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 144
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

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

<210> 145
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 145
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaaatga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 146
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 146
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Met Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 147
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 147
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 148
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 149
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 149
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgaccctga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 150
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 150
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Pro Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 151
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 151
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgctg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 152
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 152
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Leu
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 153
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 153

```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaactctc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 154

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 154
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Ser Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 155
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 155
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaacata ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 156
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 156
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu His Ile Arg Leu

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

<210> 157
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 157
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atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
```

gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 158
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 158
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

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

<210> 159
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 159
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
tcgcaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 160
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 161
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 161
atggcgttct cagcggacac ccctgaaatc gtttacaccc acattaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 162
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 163
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 163
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actgatgccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
```

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 164
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 165
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 165
```
atggcgttct caacggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tgtatggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 166
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 166
```
Met Ala Phe Ser Thr Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Tyr Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 167
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 167
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcgtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 168
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 168
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Arg Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 169
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 169
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatca atgctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 170
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 171
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 171
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgt tgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 172
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 172
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 173
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 173
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagtgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 174
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 174
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 175
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 175
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt gtctgacccc ggtacagtac                                  990
```

<210> 176
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 176
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
```

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

<210> 177
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 177
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct tgtctgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 178
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 178
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160

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

<210> 179
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 179
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaactatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 180
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 181
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 181
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggcttcgat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 182
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 182
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
```

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

<210> 183
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 183
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatcac tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 184
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 184
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Thr Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 185
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 185
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gtggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 186
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 186
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 187
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 187
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accttgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 188
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 188
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

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

<210> 189
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 189
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa ctcgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
```

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 190
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 191
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 191
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 192
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 192
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 193
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 193

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 194
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 194

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

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

<210> 195
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 195
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tccgctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 196
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 196
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 197
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 197
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctga cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 198
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 198
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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

<210> 199
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 199
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt ccttttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 200
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 201
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 201
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cccgttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 202
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 203
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 203
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tgcgggacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 204
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 204
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg

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

<210> 205
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 205
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa caatctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
```

tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcatt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 206
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg His Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 207
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 207
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtgcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 208
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 208
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 209
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 209
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgttgg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 210
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 211
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 211
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtc atgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 212
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 213
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 213
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatcct ggcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 214
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 214
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 215
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 215
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actggcggct gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 216
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 216
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 217
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 217
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtgttac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 218
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 218

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

<210> 219
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 219
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac catgaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 220
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 221
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 221
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgtttgg 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 222
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Trp
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 223
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 223
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacacggcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 224
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 224
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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

<210> 225
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 225
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggccgaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 226
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 226
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 227
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 227
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg agggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 228
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 228
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Glu Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 229

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 229
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc cggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 230
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 230
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110

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

<210> 231
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 231
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt caggttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 232
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 232
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Arg
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 233
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 233
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccctg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 234
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 234
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 235
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 235
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaactgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 236
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 236
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 237
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 237
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcgggt taaaaacttc cagtggggtg acctgatccg tgcaattcgg 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 238
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 238
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Arg Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Arg Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 239
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 239
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtactacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 240
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 240
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

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

<210> 241
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 241
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcgggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 242
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 242
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Arg Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 243
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 243
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac cgttaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 244
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 244
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Val Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 245
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 245
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
atggttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 246
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 246
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 247
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 247
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagctatcc gtgctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 248
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 248
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Arg Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 249
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 249
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggtctaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 250
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 250
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 251
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 251
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ctgtcttctc tgctgacccc ggtacagtac 990

<210> 252
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 252
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 253
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 253
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 254

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 254
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Tyr Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 255
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 255
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
gaggttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 256
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 256
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu

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

<210> 257
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 257
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaagacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
```

```
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcg gtgctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 258
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 258
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

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

<210> 259
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 259
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtaaggtac                                  990
```

<210> 260
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 261
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 261
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttacttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 262
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 262
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 263
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 263
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
```

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttcgg 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 264
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 264
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Arg
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 265
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 265
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgatgg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 266
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 266
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 267
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 267
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatct gggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 268
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 268
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 269
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 269
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgcttgttc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 270
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

<210> 271
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 271
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa caggctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 272
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 272
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 273
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 273
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaccgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 274
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 274
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 275
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 275
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtgcgac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 276
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 276
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
```

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

<210> 277
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 277
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcg aggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 278
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 278
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160

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

<210> 279
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 279
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctggtat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 280
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 281
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 281
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt caagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 282
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 282
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

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

<210> 283
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 283
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
```

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggggggaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 284
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 284
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Gly Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 285
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 285
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtcttac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 286
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 286
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Leu Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 287
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 287
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcg ctgctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 288
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 288
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

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

<210> 289
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 289
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
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gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctg tgctgacccc ggtacagtac 990

<210> 290
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

```
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Val Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 291
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 291
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt ggctgacccc ggtacagtac                                  990
```

<210> 292
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 292
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 293
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 293

```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaacgatca atgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 294
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 294
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
```

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

<210> 295
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 295
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atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtggtacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 296
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 296
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Gly Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 297
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 297
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctg gaccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tcggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 298
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 298
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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

<210> 299
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 299
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacccagt ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 300
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 301
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 301
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atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
agccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 302
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 302
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Ser Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 303
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 303
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacccagt ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
agccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagtaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 304
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 304
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Gln Phe Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Ser Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg

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

<210> 305
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 305
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaacgatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
```

tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 306
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 306
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Phe Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Thr Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 307
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 307
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacccagt ctgactacga actgatgccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 308
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 308
```
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Gln Ser Asp Tyr Glu Leu Met Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 309
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 309
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
agccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tcggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 310
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 310
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Ser Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

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

<210> 311
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 311
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacccagt ttgactacga actgatgccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 312
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 312
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Gln Phe Asp Tyr Glu Leu Met Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 313
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 313
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttcggtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 314
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 314
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Gly Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 315
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 315
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atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
```

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgtggtacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 316
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 316
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Phe Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Gly Thr Val Leu Glu Ile Ala Glu

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

<210> 317
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 317
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctcgaat gcggaatcta ttcggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 318
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 318

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

<210> 319
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 319
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgtggtacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 320
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 320
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe

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

<210> 321
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 321
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacccagt ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tcggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaacgatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 322
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 322
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Gln Phe Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Leu Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Thr Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 323
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 323
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggacaca 60
atcacctact ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
agccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtggtacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 324
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 324
```
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Tyr Phe Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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

<210> 325
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 325
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctg gaccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagtaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 326
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 326
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Gly Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 327
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 327
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgttcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctg gaccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaacgatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 328
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 328
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Phe Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Phe Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Gly Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Thr Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 329

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 329
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ttgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 330
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 330
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Phe Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110

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

<210> 331
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 331
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 332
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 332
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 333
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 333
```
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttcggtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
agccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 334
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 334
```
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 335
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 335
atggcgttct cagcggacac ccctactatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaaacgatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 336
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 336
Met Ala Phe Ser Ala Asp Thr Pro Thr Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 337
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 337
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact cggactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggctgat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 338
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 338
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Leu Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 339
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 339
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttggg ccggtaacgc tttccgtctg 240
ggggatcaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt tgctgacccc ggtacagtac 990

<210> 340
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 340
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Ala Gly Asn Ala Phe Arg Leu

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

<210> 341
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 341
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact cggactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
gtatcttctt tgctgacccc ggtacagtac 990

<210> 342
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 342
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 343
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 343
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acattaccgg tctggactat 60
atcacctacc cggacccgga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaaatga ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt tgctgacccc ggtacagtac                                  990
```

<210> 344
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 344
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Ile Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Pro Asp Pro Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Met Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Leu
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 345
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 345
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggaccat 60
atcacctact cggactatga actggacccg gctaacctgc tggctggtgg tgctgcttgg 120
atcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga atggtaacgc tttccgtctg 240
ggggatcaca tcgaacgtct gttctctaat gcggaatcta ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccagttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt tgctgacccc ggtccagtac 990

<210> 346
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 346
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp His Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 347
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 347
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgataccgg tctggactat 60
atcacctact cggactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaaatga ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggctgat cgtaccgttc 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt gtctgacccc ggtacagtac 990

<210> 348
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 348
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Met Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Leu Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Cys Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 349
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 349
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acattatcgg tcgggaccat 60
atcacctact cggactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaaatga ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt tgctgacccc ggtacagtac                                  990
```

<210> 350
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 350
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Ile Ile
1               5                   10                  15
Gly Arg Asp His Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 351
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 351
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaaatga ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatcag ggcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
gtatcttctt gtctgacccc ggtacagtac 990

<210> 352
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 352
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Met Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 353
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 353
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaaatga ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt gtctgacccc ggtacagtac                                  990
```

<210> 354

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 354
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Met Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Cys Leu Thr Pro Val Gln Tyr
                325   330

<210> 355
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 355
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgataccgg tctggaccat 60
atcacctact cggactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatcag ggcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccatcttctt gtctgacccc ggtacagtac   990

<210> 356
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 356
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp His Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu

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

<210> 357
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 357
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggaccat 60
atcacctacc cggactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaatcta ttaggttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480

```
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatcac ggcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 358
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 358
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp His Ile Thr Tyr Pro Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Thr Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

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

<210> 359
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 359
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
gggtcacaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg acggtattac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gagctgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 360
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 360
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Ser His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Asp Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 361
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 361
atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcagtaat gcggaatcca ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtcttac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 362
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 362
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 363
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 363
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atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcaggtgg cgctgcttgg 120
attggaggtg cttttgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcca ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtcctcaagt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtattac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct tgcctgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 364
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 364
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Cys Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 365
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 365
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtcctgccgt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg acggtattac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 366
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 366
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 367
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 367
atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggatcaca tcgaacgtct gttccagaat gcggaatcca ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtcttac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 368
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 368
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 369
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 369
```
atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
gggtcacaca tcgaacgtct gttccagaat gcggaatcca ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtattac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 370
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 370
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Ser His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 371
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 371
atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg cgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcagtaat gcggaatcca ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctgtg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtattac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gagctgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggttttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 372
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 372
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Val Glu Leu

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

<210> 373
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 373
```
atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttagttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggatcaca tcgaacgtct gttccagaat gcggaacata ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgagggaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
```

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtattac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gagctgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 374
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 374
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Leu Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu His Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 375
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 375
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actgaagccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcca ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 376
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 376
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
```

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

<210> 377
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 377
atggcgttct cagcggacac ccctcacatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaacata ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgagggaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accatgcatc gtcctcaagt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtcttac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gagctgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 378
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 378
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu His Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Met His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160

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

<210> 379
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 379
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccat actggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac                                  990
```

<210> 380
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 380
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Ile Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Val
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu

305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 381
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 381
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccat actggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 382
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 382
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Ile Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

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

<210> 383
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 383
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgcatt ctaggtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgctttttga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
```

acccaggacg aagttaaaga gatcgctttg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
tattcttctc tgctgacccc ggtacagtac 990

<210> 384
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 384
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr His Ser Arg Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Leu Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 385
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 385
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 386
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 386
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 387
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 387
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgattacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accctgcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
tattcttctc tgctgacccc ggtacagtac 990

<210> 388
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 388
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

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

<210> 389
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 389
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccat actggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tttggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatctttga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctttg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac 990

<210> 390
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 390
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Ile Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Phe Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

```
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 391
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 391
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctgattacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120
attaccggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 392
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 392
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 393
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 393

atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg tagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 394
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 394
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Val Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

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

<210> 395
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 395
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcctgtatt ctgattacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 396
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 396
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Leu Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 397
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 397
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcctgtatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggcgaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctttg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 398
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 398
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Leu Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

```
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Val
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 399
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 399
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
accctggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 400
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

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

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

<210> 401
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 401
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgcatt ctaggtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
accctggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accctgcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac                                  990
```

<210> 402
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 402
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr His Ser Arg Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Leu Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Leu His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 403
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 403
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgattcggga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 404
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 404
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Arg Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg

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

<210> 405
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 405
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgcatt ctgattacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
accctggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
```

tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac 990

<210> 406
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 406
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr His Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Leu Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 407
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 407
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
tattcttctc tgctgacccc ggtacagtac                                  990
```

<210> 408
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 408
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 409
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 409
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctaggtacga actggacccg gctaacccac tggctggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac 990

<210> 410
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 410
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Val
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

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

<210> 411
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 411
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgcatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
tattcttctc tgctgacccc ggtacagtac                                  990
```

<210> 412
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 412
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr His Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Tyr Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 413
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 413
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctaggtacga actggacccg gctaacatgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac   990

<210> 414
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 414
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Arg Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Met Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 415
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 415
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacgtatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tttggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatttttga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
accctggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
```

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac 990

<210> 416
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 416
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Phe Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Leu Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 417
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 417
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaagcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
tattcttctc tgctgacccc ggtacagtac                                  990
```

<210> 418
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 418

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

<210> 419
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 419
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcctgtatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggcgaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
accctggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccagttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccctcttctc tgctgacccc ggtacagtac 990

<210> 420
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 420
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Leu Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Leu Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe

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

<210> 421
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 421
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccat actggactat 60
atcacgtatt ctgattacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggcgaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccctcttctc tgctgacccc ggtacagtac 990

<210> 422
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 422
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Ile Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Val
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 423
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 423
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgacag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 424
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 424
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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

<210> 425
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 425
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 426
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 426
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 427
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 427
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cctcttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ctggtgtaac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 428
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 428
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Leu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Val Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 429

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 429
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagtgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 430
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 430
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110

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

<210> 431
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 431
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtattac catgaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcgatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg gcggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 432
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 432
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Met Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 433
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 433
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtgtaac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg ccggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt tgctgacccc ggtacagtac                                  990
```

<210> 434
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 434
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 435
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 435
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgctatg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtattac catgaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 436
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 436
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Met Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 437
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 437

```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt tgctgacccc ggtacagtac                                  990
```

<210> 438
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 438
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Leu Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

```
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 439
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 439
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 440
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 440
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
```

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

<210> 441
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 441
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtattac catgaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt tgctgacccc ggtacagtac 990

<210> 442
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 442
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 443
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 443
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtgtaac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gcggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 444
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 444
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Val Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 445
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 445
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg gcggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 446
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 446
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 447
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 447
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagtgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt ggctgacccc ggtacagtac 990

<210> 448
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 448
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Val Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Trp Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 449
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 449
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 450
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 450
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 451
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 451
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 452
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 452
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 453
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 453
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctga ctggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagtgatcc tggctgacat caccccggct gaactgacag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 454

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 454
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Thr Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Val Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Thr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 455
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 455
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgaccatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ctggtgtaac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcgatcc tggctgacat caccccggct gaactgacag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 456
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 456
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu

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

<210> 457
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 457
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
```

```
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgacag acgctgacga agtcctgggt 840
tgctcaaccg ccggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 458
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 458
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

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

<210> 459
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 459
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgacag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 460
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 460
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Thr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 461
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 461
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 462
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 462
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 463
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 463
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagtgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
```

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 464
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 464
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Val Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 465
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 465
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtattac catgaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 466
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 466
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 467
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 467
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtgtaac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 468
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 468
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 469
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 469
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctcgaac gcggaatcga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 470
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 470
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Leu Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Val Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 471
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 471
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 472
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 472
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 473
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 473
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 474
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 474
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Leu Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 475
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 475
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt tgctgacccc ggtacagtac                                  990
```

<210> 476
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 476
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
```

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

<210> 477
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 477
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 478
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 478
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Leu Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160

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

<210> 479
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 479
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tggtgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 480
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 480
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Gly Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu

305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 481
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 481
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt tgctgacccc ggtacagtac 990

<210> 482
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 482
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

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

<210> 483
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 483
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
```

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgctggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcgatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctt tgctgacccc ggtacagtac 990

<210> 484
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 484
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Leu Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 485
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 485
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg taaggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcgatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 486
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 486
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Lys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 487
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 487
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgctatg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cctcttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 488
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 488
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Met Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

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

<210> 489
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 489
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggccgaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
```

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 490
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 490
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Pro Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

```
Val Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 491
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 491
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactatga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ctggtgtaac catgaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactggtcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 492
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 492
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 493
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 493

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tcttgactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcctctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc tgggtattac caggaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgacag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 494
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 494
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
```

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

<210> 495
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 495
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tgggcggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acctagataa ccggctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaacgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 496
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 496
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Gly Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Leu Asp Asn Arg Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Pro Gly Ile Thr Arg Thr Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 497
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 497
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtat 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acctaggtaa ccggctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 498
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 498
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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

<210> 499
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 499
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat ccccccgctg 300
ttacaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
```

accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtat 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgaattgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg aaggtatcac ccgaatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 500
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 500
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Leu Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg

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

<210> 501
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 501
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acaccaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggtgataa ccggctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 502
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 502
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Thr Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Arg Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Lys Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 503
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 503
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggccggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgcgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgaattgccg ctgctgctgg acggggacaa ccggctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 504
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 504
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg

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

<210> 505
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 505
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ccaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acctaggtaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
```

tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 506
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 506
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Leu Gly Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Met Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 507
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 507
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ccaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 508
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 508
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 509
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 509
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tgggcggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat ccccccgctg 300
actcaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggtgataa ccggctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaacgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 510
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 510
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Gly Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

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

<210> 511
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 511
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acaccaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tagcggatat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 512
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 512
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Thr Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Met Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Lys Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 513
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 513
atggcgttct cagcggacac ccctgaaatc gtttacaccc acaccaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tgggcggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 514
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 514
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Thr Thr
1   5   10   15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Gly Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 515
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 515
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggccggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat ccccccgctg 300
actcaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtat 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
```

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc ccggtatcac ccgaaagacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgaagg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 516
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 516
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 517
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 517
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 518
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 518
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Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
```

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

<210> 519
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 519
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaaatga ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gtggtatcac ccgtatgacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 520
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 520
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Met Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Val
145   150   155   160

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

<210> 521
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 521
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcatgaat gcggaaatga ttcgtttgat cccgccgctg 300
agccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gtggtatcac ccgtaagacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 522
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 522
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Met Asn Ala Glu Met Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Ser Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu

305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 523
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 523
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgatgggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgc 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 524
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 524
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Met Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

```
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 525
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 525
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaatg gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 526
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 526
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 527
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 527
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
gctaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 528
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 528
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Ala Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 529
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 529
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaatcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 530
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 530
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

```
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Asn His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 531
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 531
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatg 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
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gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 532
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 532
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Met Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

```
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 533
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 533
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
gcttcttctc tgctgacccc ggtacagtac                                  990
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<210> 534
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 534
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
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            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Ala Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 535
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 535

atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaacg tatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 536
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 536
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Arg Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

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

<210> 537
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 537
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atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctcgtc tgctgacccc ggtacagtac                                  990
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<210> 538
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 538
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Arg Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 539
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 539
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaacac gatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 540
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 540
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

```
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Thr Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 541
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 541
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
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accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt taggctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 542
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 542
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val Arg Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg

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

<210> 543
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 543
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtgtttc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 544
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 544
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Val Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 545
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 545
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gttacggttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 546
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 546
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg

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

<210> 547
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 547
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacagt 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
```

tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 548
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 548
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ser Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 549
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 549
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgaccag tgtacagtac                                  990
```

<210> 550
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 550
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 551
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 551
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
tcttcttctc tgctgacccc ggtacagtac 990

<210> 552
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 552
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

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

<210> 553
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 553
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtcagccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 554
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 554
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Gln Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 555
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 555
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccgtcg gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 556
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 556
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 557
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 557
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatg cgccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
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agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 558
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 558
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Ala
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 559
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 559
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgaccca ggtacagtac                                  990
```

<210> 560
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 560

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

<210> 561
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 561
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
cataaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 562
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 562
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile His Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe

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

<210> 563
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 563
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtcttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 564
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 564
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Leu Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 565
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 565
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgaccca tgtacagtac                                  990
```

<210> 566
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 566
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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

<210> 567
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 567
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggacgat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 568
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 568
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Thr Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 569
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 569
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctgtgc tgctgacccc ggtacagtac                                  990
```

<210> 570
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 570
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Val Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 571

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 571
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga agggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 572
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 572
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Lys Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110

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

<210> 573
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 573
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggtgtat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 574
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 574
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Cys Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 575
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 575
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggagacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctgg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 576
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 576
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 577
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 577
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
acgtcttctc tgctgacccc ggtacagtac 990

<210> 578
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 578
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 579
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 579
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtaaggtac                                  990
```

<210> 580
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 580
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

Pro Ser Ser Leu Leu Thr Pro Val Arg Tyr
325 330

<210> 581
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 581
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctacg 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 582
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 582
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

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

<210> 583
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 583
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacctg 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 584
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 584
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Leu Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 585
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 585
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga ggggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 586
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 586

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

<210> 587
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 587
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcttgaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 588
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 588
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Leu Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 589
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 589
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga tctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 590
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 590
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Asp Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 591
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 591
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggtgg ggagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 592
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 592
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 593
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 593
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60

atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtagtttac 990

<210> 594
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 594
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 595
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 595
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tccgctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 596

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 596
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val Pro Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 597
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 597
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg gggctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 598
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 598
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu

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

<210> 599
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 599
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgcctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480

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gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 600
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 600
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Pro Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

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

<210> 601
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 601
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactt gatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 602
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 602
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Leu Ile Ser Asp Gly Val Pro Gly
290 295 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 603
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 603
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctggaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 604
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 604
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Trp Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

```
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 605
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 605
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggta cggttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 606
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 606
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Thr Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 607
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 607
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg cgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggttggtc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 608
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 608
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 609
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 609
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggta ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 610
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 610
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 611
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 611
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtacggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 612
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 612
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Thr Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 613
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 613
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaagt gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 614
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 614
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Val Ile Ala Leu Glu Leu

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

<210> 615
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 615
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacaatc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

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gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 616
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 616
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Asn Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
```

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

<210> 617
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 617
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtcaggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 618
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 618
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
```

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

<210> 619
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 619
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accagtcatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 620
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 620
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Ser His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160

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

<210> 621
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 621
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg ctgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 622
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 622
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Ala Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu

```
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 623
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 623

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacactgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 624
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 624

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

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

<210> 625
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 625
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttcgttaat gcggaatcta ttcgtttgat cccgccgctg 300
```

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 626
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 626
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Val Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly

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

<210> 627
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 627
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaat gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 628
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 628
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Met Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 629
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 629
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtatgtc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 630
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 630
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

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

<210> 631
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 631
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccttg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 632
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 632
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr Leu Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

```
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 633
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 633
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggta ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 634
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 634
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 635
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 635

atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccgagg gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 636
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 636
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

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

<210> 637
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 637
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gctggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 638
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 638
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Leu Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 639
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 639
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 640
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 640
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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

<210> 641
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 641
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtattccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 642
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 642
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg

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

<210> 643
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 643
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcctgcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gattgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccatac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 644
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 644
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Leu Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 645
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 645
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccatac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 646
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 646
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 647
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 647
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtagactac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
```

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 648
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 648
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Asp Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 649
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 649

```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccaccgctg 300
acccaggacg aagttaaaga gattgctctg caactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtagactac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 650
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 650

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

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

<210> 651
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 651
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gattgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtagactac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 652
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 652
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Asp Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 653
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 653
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gattgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccatac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 654
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 654
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 655
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 655
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcattgcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 656
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 656
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 657
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 657
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagg gggttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 658
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 658
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Gly Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 659
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 659
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtcc gtggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 660
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 660
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
```

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

<210> 661
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 661
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 662
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 662
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 663
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 663
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacact 60
atcacctact ctgactacga actgtacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgaaattcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtccagtac                                  990
```

<210> 664
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 664
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Tyr Ser Asp Tyr Glu Leu Tyr Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Lys Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

```
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330


<210> 665
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 665
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaaccgggaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 666
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 666
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
```

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

<210> 667
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 667
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcagctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 668
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 668
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val Gln Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 669
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 669
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acgcggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 670
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 670

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

<210> 671
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 671
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acactgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 672
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 672
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 673
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 673
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagcaatcc tcgctgatat caccccgcag gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 674
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 674
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Gln Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 675
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 675
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctttgc tgctgacccc ggtacagtac                                  990
```

<210> 676
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 676
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 677
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 677
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60

atcacccagt ctgactacga actggacccg gctaacccgt atgctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 678
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 678
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Tyr Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 679
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 679
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtgg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 680

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 680
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Trp
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 681
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 681
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatg tgccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt caaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 682
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 682
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu

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

<210> 683
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 683
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480

```
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggttcgccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 684
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 684
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

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

<210> 685
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 685
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggattcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 686
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 686
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Asp Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 687
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 687
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 688
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 688
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 689
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 689

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggta atttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 690
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 690
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Asn Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 691
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 691
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaacccg tctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 692
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 692
```
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 693
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 693
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgggtc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 694
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 694
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 695
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 695
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggttattc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 696
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 696
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Tyr Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 697
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 697
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccactgct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 698
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 698
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 699
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 699
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actcggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 700
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 700
Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Ser Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 701
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 701
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgt tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga aaggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggattcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcaaat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 702
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 702
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 703
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 703
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccggtc 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actctgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacggtac 990

<210> 704
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 704
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Val
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 705
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 705
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgt atgctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga aaggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggattcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gttagcgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 706
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 706
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Tyr Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Lys Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Asp Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 707
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 707
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgt tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gttaccgttg acggtaactc tatctctgac 900
ggtgtgccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 708
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 708
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

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

<210> 709
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 709
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcttgg 120
attggaggtg ctttcgtgcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccagaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccatac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctcg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctcgcc tgctgacccc tgtacagtac 990

<210> 710
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 710
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 711
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 711
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 712
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 712
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 713
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 713
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 714
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 714
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

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

<210> 715
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 715
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 716
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 716
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Val Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 717
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 717
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gggttcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 718
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 718
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 719
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 719
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60

atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga ggctgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 720
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 720
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Ala Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 721
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 721
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagtccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 722

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 722
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 723
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 723
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 724
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 724
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu

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

<210> 725
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 725
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480

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gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 726
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 726
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

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

<210> 727
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 727
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttttgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tcctggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 728
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 728
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Leu Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 729
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 729
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctactt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgc 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 730
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 730
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Thr Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 731
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 731
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 732
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 732
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Tyr Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 733
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 733

```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgattttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 734
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 734

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

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

<210> 735
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 735
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgtgcc gccctcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 736
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 736
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 737
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 737
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 738
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 738
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 739

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 739
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 740
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 740
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110

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

<210> 741
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 741
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga ggctgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac 990

<210> 742
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 742
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Ala Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 743
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 743
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 744
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 744
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 745
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 745
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 746
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 746
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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

<210> 747
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 747
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 748
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 748
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320

```
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330


<210> 749
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 749
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgtgcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 750
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 750
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
```

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

<210> 751
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 751
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctcgcc tgctgacccc ggtacagtac 990

<210> 752
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 752
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

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

<210> 753
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 753
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgtgcc gccctcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 754
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 754
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 755
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 755
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgtgcc gccctcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg taccccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 756
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 756
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125

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

<210> 757
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 757
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactctagct caccattcga ggctgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
```

gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 758
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 758
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Ala Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp

```
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 759
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 759
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccctcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactcttctt caccattcga ggctgacatc 420
accaaacatc gtccgcaggt ttacatgttt gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 760
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 760
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
```

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

<210> 761
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 761
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60

atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 762
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 762
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp

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

<210> 763
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 763
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 764

<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 764
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Val Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Tyr Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 765
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 765
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 766
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 766
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu

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

<210> 767
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 767
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480

gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac 990

<210> 768
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 768
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

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

<210> 769
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 769
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 770
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 770
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 771
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 771
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac   990

<210> 772
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 772
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140

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

<210> 773
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 773
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
```

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac 990

<210> 774
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 774
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly

```
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 775
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 775
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac                                  990
```

<210> 776
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 776
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
```

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

<210> 777
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 777
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 778
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 778
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu

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

<210> 779
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 779
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atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactctagct caccattcga ggctgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg taccccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 780
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 780
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu His Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Ala Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 781
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 781
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgtgcc gccctcggaa gctcgtatcc cgattttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttt gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 782
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 782
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu

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

<210> 783
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 783
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 784
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 784
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu His Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Val Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

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

<210> 785
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 785
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac                                  990
```

<210> 786
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 786
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
```

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

<210> 787
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 787
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac 990

<210> 788
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 788
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu His Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160

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

<210> 789
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 789
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggtta tgagttgccg ctgctgctgg acgggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 790
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 790
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Tyr Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu

305 310 315 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 791
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 791
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 792
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 792
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

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

<210> 793
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 793
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
```

```
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990


<210> 794
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 794
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu His Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
```

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

<210> 795
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 795
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgattttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 796
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 796
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                  10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125
Arg Gly Tyr Ser Thr Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 797
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 797
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgtgcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac 990

<210> 798
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 798
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr

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

<210> 799
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 799
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
```

gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctcgcc tgctgacccc ggtacagtac 990

<210> 800
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 800
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

```
Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275                 280                 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Arg Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 801
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 801
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttt gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg taccccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 802
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 802
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
```

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

<210> 803
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 803

```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgtgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 804
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 804

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

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

<210> 805
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 805
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctgcctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttt gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 806
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 806
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu His Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Thr Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr

325 330

<210> 807
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 807
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactctagct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttctagcc tgctgacccc ggtacagtac 990

<210> 808
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 808
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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

<210> 809
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 809
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttactat cacccgtggt tactcttctt caccattcga gagggacatc 420

accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tagcccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 810
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 810
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg

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

<210> 811
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 811
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tgcatggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cggttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgtgg gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtatg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 812
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 812
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu His Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Trp Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 813
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 813
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctggctgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactctacct caccattcga gagggacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt tgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgctag acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 814
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 814
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Gly Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Thr Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg

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

<210> 815
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 815
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtc agttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
```

tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 816
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 816
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Gln Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285

```
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 817
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 817
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccgttgct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 818
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 818
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
```

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

<210> 819
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 819
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgaatcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 820
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 820
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

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

<210> 821
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 821
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gtggcaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 822
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 822
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Trp Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 823
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 823
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tacgagtctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 824
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 824
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95

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

<210> 825
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 825
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
```

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atcgcgcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 826
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 826
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu

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

<210> 827
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 827
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgtttttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 828
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 828

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

<210> 829
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Variants of transaminase from Arthrobacter sp

<400> 829
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcagagc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 830
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 830
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr

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

<210> 831
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 831
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtc ttttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
```

ccttcttctc tgctgacccc ggtacagtac 990

<210> 832
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 832
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Leu Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
275 280 285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

```
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 833
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 833
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaacga gatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 834
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 834
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
```

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

<210> 835
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 835
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
agtaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 836
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 836
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Ser Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

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

<210> 837
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 837
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tgatctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 838
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 838
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115   120   125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145   150   155   160
Asp Arg Ile Arg Asp Gly Val Asp Leu Met Val Ala Gln Ser Val Arg
                165   170   175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180   185   190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
        195   200   205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210   215   220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225   230   235   240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245   250   255
Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260   265   270
Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Ala Gly Gly Val Trp
        275   280   285
Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290   295   300
Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305   310   315   320
Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325   330

<210> 839

<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 839
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tacgattctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac   990

<210> 840
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 840
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1   5   10   15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35   40   45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50   55   60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65   70   75   80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
                85   90   95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100   105   110

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

<210> 841
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 841
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
```

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
cgggcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 842
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 842
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190
Gly Asp Leu Ile Arg Ala Leu Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205
Leu Pro Leu Leu Leu Asp Gly Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240
Ala Ala Leu Gly Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255
Ser Leu Gly His Arg Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

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

<210> 843
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 843
```
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tcgtgacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 844
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 844
```
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1               5                   10                  15
```

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

<210> 845
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 845
atggcgttct cagcggacac ccctcatatc gtttacaccc acgacaccgg tctggacaca 60
atcacccagt ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttccaaaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttctt caccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt actggcagat cgtaccgtac 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcacttcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgg gaggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagcaatcc tcgctgatat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg caggtggtgt ttggccgttc gtttctgttg acggtaaccg tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 846
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of transaminase from Arthrobacter sp

<400> 846
Met Ala Phe Ser Ala Asp Thr Pro His Ile Val Tyr Thr His Asp Thr
1 5 10 15
Gly Leu Asp Thr Ile Thr Gln Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80
Gly Asp His Ile Glu Arg Leu Phe Gln Asn Ala Glu Ser Ile Arg Leu
85 90 95
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125
Arg Gly Tyr Ser Ser Ser Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Trp Gln Ile Val Pro Tyr
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

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