

Sequence listing(OPA18570)

<110> CJ CheilJedang Corporation  
 <120> Modified homoserine dehydrogenase and method for producing  
 homoserine or L-amino acid derived from homoserine using the same  
 <130> OPA18570  
 <150> KR 10-2018-0060445  
 <151> 2018-05-28  
 <160> 50  
 <170> KoPatentIn 3.0  
 <210> 1  
 <211> 445  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> homoserine dehydrogenase

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

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195                      200                      205  
Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
210                      215                      220  
Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
225                      230                      235                      240  
Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
245                      250                      255  
Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
260                      265                      270  
Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
275                      280                      285  
Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
290                      295                      300  
Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
305                      310                      315                      320  
Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
325                      330                      335  
Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
340                      345                      350  
Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
355                      360                      365  
Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala  
370                      375                      380  
Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu  
385                      390                      395                      400  
Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu  
405                      410                      415  
Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
420                      425                      430  
Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp  
435                      440                      445

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<213> Artificial Sequence

<220>  
<223> thrB gene

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|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gtggaaatta ttccatctgg ctggaagtg gaagttttg gcgaaggcca aggcgaagtc    | 180 |
| cctcttgatg gctccacact ggtggttaa gctattcgtg ctggcctgaa ggcagctgac   | 240 |
| gctgaagttc ctggattgcg agtgggtgtg cacaacaaca ttccgcagtc tcgtggtctt  | 300 |
| ggctcctcig ctgcagcggc ggttgctggt gttgctgcag ctaatggtt ggccgatttc   | 360 |
| ccgctgactc aagagcagat tgttcagttg tcctctgcct ttgaaggcca cccagataat  | 420 |
| gctgcgggctt ctgtgctggg tggagcagtg gtgtcgtgga caaatctgtc tatcgacggc | 480 |
| aagagccagc cacagtatgc tgctgtacca ctgaggtgc aggacaatat tcgtgcgact   | 540 |
| gcgctgggtc ctaattcca cgcattccacc gaagctgtgc gccgagtcct tcccactgaa  | 600 |
| gtcactcaca tcgatgcgcg attaacgtg tcccgcgttg cagtgatgat cgttgcgttg   | 660 |
| cagcagcgtc ctgatttgc gtgggagggt actcgtgacc gtctgcacca gccttatcgt   | 720 |
| gcagaagtgt tgcctattac ctctgagtgg gtaaaccgcc tgcgcaaccg tggctacgcg  | 780 |
| gcataccttt ccggtgccgg cccaaccgcc atggtgctgt cactgagcc aattccagac   | 840 |
| aaggtttgg aagatgctcg tgagtctggc attaagggtc ttgagcttga ggttgcggga   | 900 |
| ccagtcaagg ttgaagttaa ccaaccttag                                   | 930 |

<210> 3  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 3  
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<210> 4  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 4  
 caacgacaaa cgcccatc 18

<210> 5  
 <211> 2778  
 <212> DNA  
 <213> Artificial Sequence

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<220>

<223> gene fragment

<400>

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agagtttttc cgttgaaaac taaaaagctg ggaagggtgaa tcgaatttcg gggctttaa      180
gcaaaaatga acagcttggt ctatagtggc taggtaccct tttgttttg gacacatgta      240
gggtggccga acaaagtaa taggacaaca acgctcgacc gcgattattt ttggagaatc      300
atgacctcag catctgcccc aagctttaac cccggcaagg gtcccggctc agcagtcgga      360
attgcccttt taggattcgg aacagtcggc actgagggtga tgcgtctgat gaccgagtac      420
ggtgatgaac ttgcgcaccg cattggtggc cacttgaggg ttctggcat tgctgtttct      480
gatatctcaa agccacgtga aggcgttgca cctgagctgc tactgagga cgcttttgca      540
ctcatcgagc gcgaggatgt tgacatcgtc gttgagggtta tcggcggcat tgagtaccca      600
cgtgaggtag ttctgcagc tctgaaggcc ggcaagtctg ttgtaccgc caataaggct      660
cttgttcag ctactctgc tgagcttgct gatgcagcgg aagccgcaa cggtgacctg      720
tacttcgagg ctgctgttc aggcgcaatt ccagtggttg gccactgcg tcgtccctg      780
gctggcgatc agatccagtc tgtgatgggc atcgtaacg gcaccaccaa ctcatcttg      840
gacgccatgg attccaccgg cgctgactat gcagattctt tggctgaggc aactcgttg      900
ggttacgccg aagctgatcc aactgcagac gtcgaaggcc atgacgccgc atccaaggct      960
gcaattttgg catccatcgc ttccacacc cgtgttaccg cggatgatgt gtactgcgaa     1020
ggtatcagca acatcagcgc tgccgacatt gaggcagcac agcaggcagg ccacaccatc     1080
aagttgttgg ccatctgtga gaagtcacc aacaaggaag gaaagtcggc tatttctgct     1140
cgcgtgcacc cgactctatt acctgtgtcc caccactgg cgtcggtaaa caagtcctt     1200
aatgcaatct ttgtgaagc agaagcagct ggtcgccctga tgttctacgg aaacggtgca     1260
ggtggcgcgc caaccgcgtc tgctgtgctt ggcgacgtcg ttggtgccgc acgaaacaag     1320
gtgcacgggtg gccgtgctcc aggtgagtc accctacgcta acctgccgat cgctgatttc     1380
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gctgaattgg ctagcctgtt ctctgagcaa ggaatctccc tgcgtacaat ccgacaggaa     1500
gagcgcgatg atgatgcacg tctgatcgtg gtcaccact ctgcgctgga atctgatctt     1560
tccgcaccg ttgaactgct gaaggctaag cctgttgta aggcaatcaa cagtgtgatc     1620
cgctcgaaa gggactaatt ttactgacat ggcaattgaa ctgaacgtcg gtcgtaagg     1680

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| taccgtcacg gtacctggat cttctgcaaa cctcggacct ggctttgaca ctttaggttt | 1740 |
| ggcactgtcg gtatacgaca ctgtcgaagt ggaaattatt ccactcggct tggaaagtga | 1800 |
| agttttggc gaaggccaag gcgaagtccc tcttgatggc tcccacctgg tggtaaagc   | 1860 |
| tattcgtgct ggcctgaagg cagctgacgc tgaagttcct ggattgcgag tgggtgcca  | 1920 |
| caacaacatt ccgcagtctc gtggtcttgg ctctctgct gcagcggcgg ttgctggtgt  | 1980 |
| tgctgcagct aatggtttgg cggatttccc gctgactcaa gagcagattg ttcagttgtc | 2040 |
| ctctgccttt gaaggccacc cagataatgc tgcggcttct gtgctgggtg gagcagtgtt | 2100 |
| gtcgtggaca aatctgtcta tcgacggcaa gagccagcca cagtatgctg ctgtaccact | 2160 |
| tgagggtcag gacaatattc gtgcgactgc gctggttctt aatttcacg catccaccga  | 2220 |
| agctgtgcgc cgagtccttc ccactgaagt cactcacatc gatgcgcgat ttaacgtgtc | 2280 |
| ccgcgttgca gtgatgatcg ttgcgttgca gcagcgtcct gatttgctgt gggagggtag | 2340 |
| tcgtgaccgt ctgcaccagc cttatcgtgc agaagtgttg cctattacct ctgagtgggt | 2400 |
| aaaccgcctg cgcaaccgtg gctacgcggc atacctttcc ggtgccggcc caaccgccat | 2460 |
| gggtctgtcc actgagccaa ttccagacaa ggttttggaa gatgctctg agtctggcat  | 2520 |
| taagggtgctt gagcttgagg ttgcgggacc agtcaagggt gaagtaacc aaccttaggc | 2580 |
| ccaacaagga agggccctt cgaatcaaga agggggcctt attagtgcag caattattcg  | 2640 |
| ctgaacacgt gaaccttaca ggtgcccgcc gcgttgagtg gtttgagttc cagctggatg | 2700 |
| cggttgtttt caccgaggct ttcttggatg aatccggcgt ggatggcgca gacgaaggct | 2760 |
| gatgggcggt tctcgttg                                               | 2778 |

<210> 6  
 <211> 1338  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> T285I

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 6                                                            |     |
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| attgcccttt taggattcgg aacagtcggc actgagggtga tgcgtctgat gaccgagtag | 120 |
| gggtatgaac ttgcgcaccg cattgggtggc ccactggagg ttctggcat tgctgtttct  | 180 |
| gatatctcaa agccacgtga aggcgttgca cctgagctgc tcaactgagga cgcttttgca | 240 |
| ctcatcgagc gcgaggatgt tgacatcgtc gttgagggtta tcggcggcat tgagtaccca | 300 |
| cgtgaggtag ttctcgagc tctgaaggcc ggcaagtctg ttgtaccgc caataaggct    | 360 |

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| ctgttgacag ctactctgc tgagcttgct gatgcagcgg aagccgcaa cgttgacctg   | 420  |
| tacttcgagg ctgctgttc aggcgcaatt ccagtgggtg gccactgcg tcgctccctg   | 480  |
| gctggcgatc agatccagtc tggatgggc atcgtaacg gcaccacaa ctcatcttg     | 540  |
| gacgccatgg attccaccgg cgctgactat gcagattctt tggctgaggc aactcgttg  | 600  |
| ggttacgccg aagctgatcc aactgcagac gtcgaaggcc atgacgccgc atccaaggct | 660  |
| gcaattttgg catccatcgc ttccacacc cgtgttaccg cggatgatgt gtactgcgaa  | 720  |
| ggatcagca acatcagcgc tgccgacatt gaggcagcac agcaggcagg ccacaccatc  | 780  |
| aagttgttg ccatctgtga gaagtcacc aacaaggaag gaaagtcggc tattctgct    | 840  |
| cgctgcacc cgattctatt acctgtgtcc caccactgg cgtcggtaaa caagtcctt    | 900  |
| aatgcaatct ttgtgaagc agaagcagct ggtcgctga tgtctacgg aaacgggtga    | 960  |
| ggtggcgccg caaccgcgc tgctgtgctt ggcgacgtcg ttggtgccg acgaaacaag   | 1020 |
| gtgcacgggt gccgtgtcc aggtgagtc acctacgcta acctgccgat cgctgattc    | 1080 |
| ggtgagacca ccactcgta ccacctgcac atggatgtgg aagatcgct gggggtttg    | 1140 |
| gctgaattgg ctacgtgtt ctctgagcaa ggaatctccc tgcgtacaat ccgacaggaa  | 1200 |
| gagcgcgatg atgatgcacg tctgatcgtg gtcaccact ctgcgtgga atctgatctt   | 1260 |
| tcccgaccg ttgaactgct gaaggctaag cctgtgttta aggcaatcaa cagtgtgatc  | 1320 |
| cgctcgaaa gggactaa                                                | 1338 |

<210> 7  
 <211> 1338  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> R398Q

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 7                                                           |     |
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| attgcccttt taggattcgg aacagtcggc actgaggta tgcgtctgat gaccgagtac  | 120 |
| ggtgatgaac ttgcgcaccg cattggtggc ccactggagg ttctggcat tgctgtttct  | 180 |
| gatatctcaa agccacgtga aggcgttgca cctgagctgc tactgagga cgcttttgca  | 240 |
| ctcatcgagc gcgaggatgt tgacatcgtc gttgaggta tcggcggcat tgagtaccca  | 300 |
| cgtgaggtag ttctgcagc tctgaaggcc ggcaagtctg ttgtaccgc caataaggct   | 360 |
| ctgttgacag ctactctgc tgagcttgct gatgcagcgg aagccgcaa cgttgacctg   | 420 |
| tacttcgagg ctgctgttc aggcgcaatt ccagtgggtg gccactgcg tcgctccctg   | 480 |

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| gctggcgatc agatccagtc tgtgatgggc atcgtaacg gcaccaccaa ctcatcttg   | 540  |
| gacgccatgg attccaccgg cgctgactat gcagattctt tggctgaggc aactcgttg  | 600  |
| ggttacgccg aagctgatcc aactgcagac gtcgaaggcc atgacgccgc atccaaggct | 660  |
| gcaattttgg catccatcgc ttccacacc cgtgttaccg cggatgatgt gtactgcgaa  | 720  |
| ggtatcagca acatcagcgc tgccgacatt gaggcagcac agcaggcagg ccacaccatc | 780  |
| aagtgtgtgg ccatctgtga gaagttcacc aacaaggaag gaaagtcggc tatttctgct | 840  |
| cgcgtgcacc cgactctatt acctgtgtcc caccactgg cgtcggtaaa caagtccttt  | 900  |
| aatgcaatct ttgtgaagc agaagcagct ggtcgccctga tgttctacgg aaacggtgca | 960  |
| ggtggcgcg ccaaccgcgc tgctgtgctt ggcgacgtcg ttggtgccgc acgaaacaag  | 1020 |
| gtgcacgggtg gccgtgtcc aggtgagtc acctacgcta acctgccgat cgctgatttc  | 1080 |
| ggtgagacca cactcgta ccacctcgac atggatgtgg aagatcgct gggggtttg     | 1140 |
| gctgaattgg ctaccctgtt ctctgagcaa ggaatctccc tgcgtacaat ccaacaggaa | 1200 |
| gagcgcatg atgatgcacg tctgatcgtg gtcaccact ctgcgtgga atctgatctt    | 1260 |
| tcccgaccg ttgaactgct gaaggctaag cctgttgta aggcaatcaa cagtgtgatc   | 1320 |
| cgcctcgaaa gggactaa                                               | 1338 |

<210> 8  
 <211> 1338  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> G378W

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 8                                                           |     |
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| attgcccttt taggattcgg aacagtcggc actgaggta tgcgtctgat gaccgagtac  | 120 |
| ggtgatgaac ttgcgcaccg cattggtggc cactggagg ttctggcat tgctgtttct   | 180 |
| gatatctcaa agccacgtga aggcgttgca cctgagctgc tactgagga cgcttttgca  | 240 |
| ctcatcgagc gcgaggatgt tgacatcgtc gttgaggta tcggcggcat tgagtaccca  | 300 |
| cgtgaggtag ttctcgagc tctgaaggcc ggcaagtctg ttgtaccgc caataaggct   | 360 |
| cttgttcag ctactctgc tgagcttgct gatgcagcg aagccgcaa cgttgacctg     | 420 |
| tacttcgagg ctgctgttc aggcgcaatt ccagtgttg gccactgcg tcgtccctg     | 480 |
| gctggcgatc agatccagtc tgtgatgggc atcgtaacg gcaccaccaa ctcatcttg   | 540 |
| gacgccatgg attccaccgg cgctgactat gcagattctt tggctgaggc aactcgttg  | 600 |

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ggttacgccg aagctgatcc aactgcagac gtcgaaggcc atgacgccgc atccaaggct 660  
gcaattttgg catccatcgc ttccacacc cgtgttaccg cggatgatgt gtactgcgaa 720  
ggatcagca acatcagcgc tgccgacatt gaggcagcac agcaggcagg ccacaccatc 780  
aagttgttgg ccatctgtga gaagttcacc aacaaggaag gaaagtcggc tattctgct 840  
cgcgtgcacc cgactctatt acctgtgtcc caccactgg cgtcggtaaa caagtccttt 900  
aatgcaatct ttgtgaagc agaagcagct ggtcgctga tgtctacgg aaacgggtga 960  
ggtagcgccg caaccgcgtc tgctgtgctt ggagcagtcg ttggtgccgc acgaaacaag 1020  
gtgcacgggtg gccgtgtcc aggtgagtc accctacgcta acctgccgat cgctgatttc 1080  
ggtagacca ccactcgtta ccacctcgc atggatgtgg aagatcgct gtgggttttg 1140  
gctgaattgg ctacgtgtt ctctgagcaa ggaatctccc tgcgtacaat ccgacaggaa 1200  
gagcgcgatg atgatgcacg tctgatcgtg gtcaccact ctgcgctgga atctgatctt 1260  
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<210> 9  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> G378S

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ggtagaac ttgcgcaccg cattggtggc ccactggagg ttctggcat tgctgtttct 180  
gatatctcaa agccacgtga aggcgttgca cctgagctgc tctactgagga cgcttttgca 240  
ctatcgcagc gcgaggatgt tgacatcgtc gttgaggta tcggcggcat tgagtaccca 300  
cgtgaggtag ttctgcagc tctgaaggcc ggcaagtctg ttgtaccgc caataaggct 360  
cttgtgcag ctactctgc tgagcttgc gatgcagcg aagccgcaa cggtgacctg 420  
tacttcgagg ctgctgtgc aggcgcaatt ccagtgggtg gccactgcg tcgctccctg 480  
gctggcgatc agatccagtc tgtatgggc atcgtaacg gcaccaccaa ctcatcttg 540  
gacgccatgg attccaccgg cgctgactat gcagattctt tggctgaggc aactcgttg 600  
ggttacgccg aagctgatcc aactgcagac gtcgaaggcc atgacgccgc atccaaggct 660  
gcaattttgg catccatcgc ttccacacc cgtgttaccg cggatgatgt gtactgcgaa 720

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ggatcagca acatcagcgc tgccgacatt gaggcagcac agcaggcagg ccacaccatc 780  
aagttgttgg ccatctgtga gaagttcacc aacaaggaag gaaagtcggc ttttctgct 840  
cgcggtgcacc cgactctatt acctgtgtcc caccactgg cgtcggtaaa caagtccttt 900  
aatgcaatct ttgtgaagc agaagcagct ggtcgctga tgttctacgg aaacgggtgca 960  
ggtggcgcg ccaaccgcgtc tgctgtgctt ggcgacgtcg ttggtgccgc acgaaacaag 1020  
gtgcacgggtg gccgtgctcc aggtgagtc accctacgcta acctgccgat cgctgatttc 1080  
ggtgagacca ccactcgta ccacctcgac atggatgtgg aagatcgctg gagcgttttg 1140  
gctgaattgg ctacgctgtt cctgagcaa ggaatctccc tgcgtacaat ccgacaggaa 1200  
gagcgcgatg atgatgcacg tctgatcgtg gtcaccact ctgcgctgga atctgatctt 1260  
tccgcaccg ttgaactgct gaaggctaag cctgtgttta aggcaatcaa cagtgtgatc 1320  
cgccctgaaa gggactaa 1338

<210> 10  
<211> 445  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Hom (KFCC10881-1)

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

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145                    150                    155                    160  
Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
                         165                    170                    175  
Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
                         180                    185                    190  
Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
                         195                    200                    205  
Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
                         210                    215                    220  
Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
225                    230                    235                    240  
Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
                         245                    250                    255  
Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
                         260                    265                    270  
Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Ile Leu Leu Pro  
                         275                    280                    285  
Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
                         290                    295                    300  
Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
305                    310                    315                    320  
Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
                         325                    330                    335  
Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
                         340                    345                    350  
Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
                         355                    360                    365  
Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala  
370                    375                    380  
Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu  
385                    390                    395                    400  
Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu  
                         405                    410                    415  
Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
                         420                    425                    430  
Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp  
                         435                    440                    445

<210> 11  
<211> 445  
<212> PRT  
<213> Artificial Sequence

# Sequence listing(OPA18570)

<220>

<223> Hom (KFCC10881-14)

<400> 11

Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
1 5 10 15

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

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
35 40 45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
130 135 140

Ala Val Ala Gly Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
165 170 175

Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
180 185 190

Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
195 200 205

Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
210 215 220

Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
225 230 235 240

Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
245 250 255

Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
260 265 270

Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
275 280 285

Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe

Sequence listing(OPA18570)

290 295 300  
Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
305 310 315 320  
Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
325 330 335  
Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
340 345 350  
Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
355 360 365  
Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala  
370 375 380  
Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Gln Gln Glu  
385 390 395 400  
Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu  
405 410 415  
Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
420 425 430  
Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp  
435 440 445

<210> 12  
<211> 445  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Hom (KFCC10881-19)

<400> 12  
Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
1 5 10 15  
Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu  
20 25 30  
Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
35 40 45  
Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
50 55 60  
Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
65 70 75 80  
Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
85 90 95  
Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
100 105 110

Sequence listing(OPA18570)

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
130 135 140

Ala Val Ala Gly Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
165 170 175

Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
180 185 190

Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
195 200 205

Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
210 215 220

Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
225 230 235 240

Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
245 250 255

Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
260 265 270

Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
275 280 285

Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
290 295 300

Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
305 310 315 320

Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
325 330 335

Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
340 345 350

Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
355 360 365

Leu Asp Met Asp Val Glu Asp Arg Val Trp Val Leu Ala Glu Leu Ala  
370 375 380

Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu  
385 390 395 400

Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu  
405 410 415

Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
420 425 430

Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp

Sequence listing(OPA18570)

435

440

445

<210> 13  
<211> 445  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Hom (KFCC10881-22)

<400> 13  
Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
1 5 10 15

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

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
35 40 45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
130 135 140

Ala Val Ala Gly Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
165 170 175

Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
180 185 190

Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
195 200 205

Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
210 215 220

Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
225 230 235 240

Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
245 250 255

# Sequence listing(OPA18570)

Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
260 265 270

Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
275 280 285

Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
290 295 300

Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
305 310 315 320

Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
325 330 335

Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
340 345 350

Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
355 360 365

Leu Asp Met Asp Val Glu Asp Arg Val Ser Val Leu Ala Glu Leu Ala  
370 375 380

Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu  
385 390 395 400

Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu  
405 410 415

Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
420 425 430

Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp  
435 440 445

<210> 14  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 14  
tcgagctcgg taccctgcg acagcatgga actc 34

<210> 15  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 15  
ctctagagga tccccttagt ccccttcgag gcgg 34

# Sequence listing(OPA18570)

<210> 16  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 16  
caccggcgct gactatgc 18

<210> 17  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 17  
aatcgggtgc acgcgagc 18

<210> 18  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 18  
ttggattgta cgcagga 18

<210> 19  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 19  
ccacacgcga tcttcac 18

<210> 20  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

# Sequence listing(OPA18570)

<400> 20  
gctcacgcga tcttcac 18

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 21  
ttagtcctt tcgaggcg 18

<210> 22  
<211> 421  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> lysC(L377K)

<400> 22  
Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
1 5 10 15  
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30  
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45  
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60  
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80  
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95  
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110  
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125  
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140  
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160  
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Sequence listing(OPA18570)

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Lys Ile Ser Thr Ser Glu Ile Arg  
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
405 410 415

Ala Gly Thr Gly Arg  
420

<210> 23  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 23  
tcgagctcgg tacccgctgc gcagtgttga atac

34

# Sequence listing(OPA18570)

<210> 24  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 24  
tggaaatctt ttcgatgttc acgtgacat 30

<210> 25  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 25  
atgtcaacgt gaacatcgaa aagatttcca 30

<210> 26  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 26  
ctctagagga tccccgttca cctcagagac gatt 34

<210> 27  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 27  
acggatccca gactccaaag caaaagcg 28

<210> 28  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

# Sequence listing(OPA18570)

<400> 28  
acaccacggc agaaccaggt gcaaaggaca

30

<210> 29  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 29  
ctggttctgc cgtggtgtgc atcatctctg

30

<210> 30  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 30  
acggatccaa ccaaacttgc tcacactc

28

<210> 31  
<211> 1161  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> metB gene

<400> 31  
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ccagacgact actacggttc gattaacacc ccaatctatg cctccaccac cttcgcgag 120  
aacgctccaa acgaactgcg caaaggctac gagtacaccc gtgtgggcaa ccccaccatc 180  
gtggcattag agcagaccgt cgcagcactc gaaggcgcaa agtatggccg cgcattctcc 240  
tccggcatgg ctgcaaccga catcctgttc cgcacatcc tcaagccggg cgatcacatc 300  
gtcctcggca acgatgctta cggcggaacc taccgcctga tcgacaccgt attcaccgca 360  
tggggcgctc aatacaccgt tgttgatacc tccgtcgtgg aagagggtcaa ggcagcgatc 420  
aaggacaaca ccaagctgat ctgggtggaa accccaacca acccagcact tggcatcacc 480  
gacatcgaag cagtagcaaa gctcaccgaa ggcaccaacg ccaagctggt tgttgacaac 540  
accttcgcat ccccatacct gcagcagcca ctaaaactcg gcgcacacgc agtctctcac 600

# Sequence listing(OPA18570)

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tccaccacca agtacatcgg aggacactcc gacgttggtg ggggccttgt ggttaccaac      660
gaccaggaaa tggacgaaga actgctgttc atgcagggcg gcatcggacc gatcccatca      720
gttttcgatg catacctgac cgcccgtggc ctcaagaccc ttgcagtgcg catggatcgc      780
cactgcgaca acgcagaaaa gatcgcggaa ttctggact cccgcccaga ggtctccacc      840
gtgctctacc caggctgaa gaaccaccca ggccacgaag tcgcagcgaa gcagatgaag      900
cgcttcggcg gcatgatctc cgtccgttc gcaggcggcg aagaagcagc taagaagttc      960
tgtacctcca ccaaactgat ctgtctggcc gagtccctcg gtggcgtgga atccctcctg     1020
gagcaccag caaccatgac ccaccagtca gctgccggct ctacgctcga ggttccccgc     1080
gacctcgtgc gcatctccat tggattgaa gacattgaag acctgctcgc agatgtcgag     1140
caggccctca ataaccttta g                                         1161
```

```
<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> primer
```

```
<400> 32
tctagacgcc cgcatactgg cttc                                         24
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```
<210> 33
<211> 37
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> primer
```

```
<400> 33
cccatccact aaacttaaac agatgtgac gcccggc                                         37
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```
<210> 34
<211> 38
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> primer
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```
<400> 34
tgtttaagtt tagtggatgg ggaagaacca cccaggcc                                         38
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# Sequence listing(OPA18570)

<210> 35  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 35  
gtcgaccaat cgtccagagg gcg 23

<210> 36  
<211> 1314  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> metY gene

<400> 36  
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gcaggccagt cagtagacgc acagaccagc gcacgaaacc ttccgatcta ccaatccacc 120  
gctttcgtgt tcgactccgc tgagcagcc aagcagcgtt tcgcacttga ggatctaggc 180  
cctgtttact cccgcctcac caacccaacc gttgaggctt tggaaaaccg catcgcttcc 240  
ctcgaagggtg gcgtccacgc ttagcgttc tctccggac aggccgcaac caccaacgcc 300  
atattgaacc tggcaggagc gggcgaccac atcgtcacct cccacgcct ctacgggtggc 360  
accgagactc tattccttat cactcttaac cgctgggta tcgatgttc cttcgtggaa 420  
aaccccgacg accctgagtc ctggcaggca gccgttcagc caaacaccaa agcattcttc 480  
ggcgagactt tcgccaaccc acaggcagac gtctggata ttctgcggt ggctgaagtt 540  
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cgcccgctcg agtcgggcgc agacgttgc gtgcgttccc tcaccaagtt ctacaccggc 660  
aacggctccg gactgggcgg cgtgcttacc gacggcggaa agttcgattg gactgtcgaa 720  
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aagtacgcag accttggtgc accagccttc ggcctcaagg ttgcggttg cttctacgc 840  
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ctttccctgc gcctggagcg ccacaacgaa aacgccatca aggttcgaga attcctcaac 960  
aaccacgaga aggtggaaaa ggtaacttc gcaggcctga aggattcccc ttggtacgca 1020  
accaaggaaa agcttggcct gaagtacacc ggctccgttc tcaccttga gatcaagggc 1080  
ggcaaggatg aggctgggc atttatcgac gcctgaagc tacactcaa ccttgcaaac 1140

# Sequence listing(OPA18570)

atcggcgatg ttcgctccct cgttggtcac ccagcaacca ccaccattc acagtccgac 1200  
gaagctggcc tggcacgccc gggcggtacc cagtccaccg tccgcctgtc cgttggcatc 1260  
gagaccattg atgatatcat cgctgacctc gaaggcggct ttgctgcaat ctag 1314

<210> 37  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 37  
tctagaccat cctgcaccat ttag 24

<210> 38  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 38  
cccatccact aaacttaaac acgctcctgc caggttc 37

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

<220>  
<223> primer

<400> 39  
tgtttaagtt tagtggatgg gcttggtagc caaccaagg 39

<210> 40  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 40  
gtcgacgatt gctccggctt cgg 23

<210> 41  
<211> 2213

# Sequence listing(OPA18570)

<212> DNA

<213> Artificial Sequence

<220>

<223> mcbR gene

<400> 41

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aaagagtgat tcatggccg agactcctaa aagttgacc tcacaggatt gcttctaagg      180
gcctctcaa tctccactga ggtacttaat ccttcgggg aattcgggcg cttaaatacga      240
gaaattaggc catcacctt taataacaat acaatgaata attggaatag gtcgacacct      300
ttggagcgga gccggttaa attggcagca ttcaccgaaa gaaaaggaga accacatgct      360
tgccctaggt tggattacat ggaacattat tgggtgctc gctggttga ttgcctcaa      420
gattaaaggc actgatgctc agcaaggaat ttgtctgaac atagtcgtcg gtattatcgg      480
tggtttgta ggcggctggc tgcttgaat ctccggagt gatgtgccg gtggcggctt      540
gatcttcagc tcatcacat gtctgattgg tgctgtcatt ttgtgacga tcgtgcagtt      600
cttactcgg aagaagtaat ctgctttaa tccgtagggc ctgttgatat ttcgatatca      660
acaggccttt tggatcttt ggggtgaaa aagcgctaga ctgcctgtg gattaaaact      720
atacgaaccg gttgtctat attggtgta gacagttcgt cgtatctga aacagaccaa      780
cccgaaggga cgtggccgaa cgtggctgct agcgcttcag gcaagagtaa aacaagtgcc      840
ggggcaaacc gtcgtcgaa tcgaccaagc ccccgacagc gtctcctga tagcgcaacc      900
aacctttca ccacagaagg tattcgctc atcggattg atcgtatcct ccgtgaagct      960
gacgtggcga aggcgagcct ctattccct ttccgatcga aggacgcctt ggttattgca     1020
tacctggaga acctcgatca gctgtggcgt gaagcgtggc gtgagcgcac cgtcggtatg     1080
aaggatccgg aagataaaat catcgcttc ttgatcagt gcattgagga agaaccagaa     1140
aaagatttcc gcggctcga cttcagaat gcggctagt agtaccctcg ccccgaaact     1200
gatagcgaag agggcattgt tgcagcagt ttagagcacc gcgagtggg tcataagact     1260
ctgactgatt tgctactga gaagaacggc taccaggga ccaccaggc gaatcagctg     1320
ttggtgttcc ttgatggtg acttgctgga tctgattgg tccacaacat cagtctctt     1380
gagacggctc gcgattggc tcggcagttg ttgcggctc cacctcgga ctactcaatt     1440
tagttcttc attttccgaa ggggtatct cgtggggga ggcgtcgata agccccttct     1500
tttagcttt aacctcagc cgacgctgt ttaagcgtg catggcggcg cggttcattt     1560
cacgttgcgt ttcgcgctc ttgttcgga ttctttgcg ggcctgttt gcttcgttga     1620

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# Sequence listing(OPA18570)

```

tttcggcagt acggggtttg gtgagttcca cgtttgtgc gtgaagcgtt gaggcgttcc      1680
atgggggtgag aatcatcagg gcgcgggttt tgcgtcgtgt ccacaggaag atgcgcgttt      1740
ctttttgttt tgcgcggtag atgtcgcgct gctctagggtg gtgcactttg aaatcgtcgg      1800
taagtgggta ttgcgttcc aaaatgacca tcatgatgat tgtttggagg agcgtccaca      1860
ggttgttgct gacccaatag agtgcgattg ctgtggggaa tggctctgtg aggccaaggg      1920
acagtgggaa gatcggcgcg aggatcgaca tcacgatcat gaacttcagc atgccgttag      1980
agaatccgga tgcgtaatcg ttggtttgga agctgcggta catggacatc gccatgttga      2040
ttgcggtgag gattgcggct gtgatgaaca gtggcaaaac gaaactaaga acttccgcct      2100
gcgtggtgct caaatatfff agctgctcag tgggcatcga aacataagcg ggcagaggca      2160
cattgctcac gcgaccagcg aggaaagatt ccacttcctc aggagttagg aag          2213

```

```

<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> primer

```

```

<400> 42
ggccccgggcc tgcctgggtt gtcttgta          28

```

```

<210> 43
<211> 35
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> primer

```

```

<400> 43
cggaatatga agaaagttcg gccacgtcct ttccg          35

```

```

<210> 44
<211> 35
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> primer

```

```

<400> 44
aggacgtggc cgaactttct tcattttccg aaggg          35

```

# Sequence listing(OPA18570)

<210> 45  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 45  
atccccggggt ttcgatgccc actgagca 28

<210> 46  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 46  
aatctggatt tccgccaggt 20

<210> 47  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 47  
cttcctaact cctgaggaag 20

<210> 48  
<211> 1338  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> wild-type hom gene

<400> 48  
atgacctcag catctgcccc aagctttaac cccggcaagg gtccccggctc agcagtcgga 60  
attgcccttt taggattcgg aacagtcggc actgagggtga tgcgtctgat gaccgagtac 120  
ggatgatgaac ttgcgcaccg cattggtggc cacttgaggg ttcgtggcat tgctgtttct 180  
gatatctcaa agccacgtga aggcgttgca cctgagctgc tactgagga cgcttttgca 240  
ctcatcgagc gcgaggatgt tgacatcgtc gttgagggtta tcggcggcat tgagtaccca 300  
cgtgaggtag ttctgcgagc tctgaaggcc ggcaagtctg ttgtlaccgc caataaggct 360

Sequence listing(OPA18570)

cttgttcag ctactctgc tgagcttgct gatgcagcgg aagccgcaa cggtgacctg 420  
tacttcgagg ctgctgttc aggcgcaatt ccagtggttg gccactgcg tcgctccctg 480  
gctggcgatc agatccagtc tgtgatgggc atcgtaacg gcaccaccaa ctcatcttg 540  
gacgccatgg atccaccgg cgctgactat gcagattctt tggctgaggc aactcgttg 600  
ggttacgccg aagctgatcc aactgcagac gtcgaaggcc atgacgccgc atccaaggct 660  
gcaattttgg catccatcgc ttccacacc cgtgttaccg cggatgatgt gtactgcgaa 720  
ggatcagca acatcagcgc tgccgacatt gaggcagcac agcaggcagg ccacaccatc 780  
aagttgttg ccatctgtga gaagtcacc aacaaggaag gaaagtcggc tattctgct 840  
cgcgtgcacc cgactctatt acctgtgtcc caccactgg cgtcggtaaa caagtcctt 900  
aatgcaatct ttgtgaagc agaagcagct ggtcgcctga tgtctacgg aaacggtgca 960  
ggtgccgcgc caaccgcgc tgctgtgctt ggcgacgtcg ttggtgccgc acgaaacaag 1020  
gtgcacgggtg gccgtgctcc aggtgagtc acctacgcta acctgccgat cgctgattc 1080  
ggtagacca ccactcgta ccacctcgac atggatgtgg aagatcgct gggggtttg 1140  
gctgaattgg ctgacctgt ctctgagcaa ggaatctccc tgcgtacaat ccgacaggaa 1200  
gagcgcgatg atgatgcacg tctgatcgtg gtcaccact ctgcgtgga atctgatctt 1260  
tcccgaccg ttgaactgct gaaggctaag cctgttgta aggcaatcaa cagtgtgatc 1320  
cgctcgaaa ggactaa 1338

<210> 49  
<211> 445  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ATCC14067 hom (NCgl1136)

<400> 49  
Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
1 5 10 15  
Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu  
20 25 30  
Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
35 40 45  
Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
50 55 60  
Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
65 70 75 80  
Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly

Sequence listing(OPA18570)

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 85                                                              | 90  | 95  |
| Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys |     |     |
| 100                                                             | 105 | 110 |
| Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu |     |     |
| 115                                                             | 120 | 125 |
| Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala |     |     |
| 130                                                             | 135 | 140 |
| Ala Val Ala Gly Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu |     |     |
| 145                                                             | 150 | 155 |
| Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr |     |     |
| 165                                                             | 170 | 175 |
| Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp |     |     |
| 180                                                             | 185 | 190 |
| Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr |     |     |
| 195                                                             | 200 | 205 |
| Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala |     |     |
| 210                                                             | 215 | 220 |
| Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu |     |     |
| 225                                                             | 230 | 235 |
| Gly Ile Ser Asn Ile Ser Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala |     |     |
| 245                                                             | 250 | 255 |
| Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys |     |     |
| 260                                                             | 265 | 270 |
| Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro |     |     |
| 275                                                             | 280 | 285 |
| Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe |     |     |
| 290                                                             | 295 | 300 |
| Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala |     |     |
| 305                                                             | 310 | 315 |
| Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala |     |     |
| 325                                                             | 330 | 335 |
| Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr |     |     |
| 340                                                             | 345 | 350 |
| Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His |     |     |
| 355                                                             | 360 | 365 |
| Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala |     |     |
| 370                                                             | 375 | 380 |
| Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu |     |     |
| 385                                                             | 390 | 395 |
| Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu |     |     |
| 405                                                             | 410 | 415 |

# Sequence listing(OPA18570)

Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val  
420 425 430

Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp  
435 440 445

<210> 50  
<211> 445  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ATCC13869 hom

<400> 50  
Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
1 5 10 15

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

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
35 40 45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
130 135 140

Ala Val Ala Ala Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
165 170 175

Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
180 185 190

Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
195 200 205

Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
210 215 220

Ser Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu

Sequence listing(OPA18570)

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